

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 02:25:09 ; Search time 2501 Seconds

(without alignments)  
15016.009 Million cell updates/sec

Title: US-08-657-449-13

Perfect score: 918  
Sequence: 1 GAATTCATGAAAAAACCGC.....ATCACCATGCTGAAGCTT 918Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank1.\*  
1: gb\_ba.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pac.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_scs.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pac.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_scs.\*  
28: em\_un.\*  
29: em\_vi.\*  
30: em\_hcg\_hum.\*  
31: em\_hcg\_inv.\*  
32: em\_hcg\_other.\*  
33: em\_hcg\_mus.\*  
34: em\_hcg\_pln.\*  
35: em\_hcg\_rod.\*  
36: em\_hcg\_mam.\*  
37: em\_hcg\_vrt.\*  
38: em\_sy.\*  
39: em\_hcgo\_hum.\*  
40: em\_hcgo\_mus.\*  
41: em\_hcgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	6 AR139128	AR139128 Sequence
2	916.4	99.8	918	6 AR139129	AR139129 Sequence
3	799.6	87.1	867	6 AR139130	AR139130 Sequence
4	798	86.9	867	6 AR139131	AR139131 Sequence
5	463.8	50.5	801	12 AF027160	AF027160 Synthetic
6	445	48.5	1630	6 AX023365	AX023365 Sequence
7	445	48.5	1630	6 AX023367	AX023367 Sequence
8	414.4	45.1	867	12 AF416910	AF416910 Synthetic
9	369.6	40.3	861	12 AF416909	AF416909 Synthetic
10	361	39.3	450	6 AR139121	AR139121 Sequence
11	359.4	39.2	450	6 AR139120	AR139120 Sequence
12	358.4	39.0	790	10 MAA05051	MAA05051 Mus muscu
13	352	38.3	790	10 MMV124FRG	MMV124FRG
14	348.4	38.0	762	6 AX601792	AX601792 Sequence
15	346.2	37.7	864	12 XXU34924	XXU34924 Synthetic
16	345.2	37.6	780	12 SYN1988CF	SYN1988CF
17	345.2	37.6	783	6 AR198737	AR198737 Sequence
18	343.6	37.4	786	6 AX601794	AX601794 Sequence
19	343.6	37.4	1848	6 I73512	I73512 Sequence
20	343.6	37.4	1848	12 U06943	U06943 Synthetic
21	342.8	37.3	771	6 AX601793	AX601793 Sequence
22	329	35.8	786	6 AX601796	AX601796 Sequence
23	327.6	35.7	765	12 AF377321	AF377321 Synthetic
24	326	35.5	888	6 AX055802	AX055802 Sequence
25	324.4	35.3	543	6 AR139118	AR139118 Sequence
26	324.4	35.3	543	6 AR139119	AR139119 Sequence
27	321.2	35.0	811	9 AB064067	AB064067 Homo sapi
28	321	34.8	735	6 E13598	E13598 DNA encodin
29	319.8	34.8	1413	6 AX616568	AX616568 Sequence
30	315	34.3	753	6 I08679	I08679 Sequence
31	314.8	34.3	833	9 AB064110	AB064110 Homo sapi
32	314.6	34.3	378	9 HSA555261	HSA555261 Homo sapi
33	313.8	34.2	829	9 AB064118	AB064118 Homo sapi
34	313.6	34.2	376	9 AB021535	AB021535 Homo sapi
35	313.6	34.2	829	9 AB064107	AB064107 Homo sapi
36	313.6	34.2	829	9 AB064108	AB064108 Homo sapi
37	313.4	34.1	379	9 AB021507	AB021507 Homo sapi
38	312.8	34.1	384	9 HSA239336	HSA239336 Homo sapi
39	310.6	33.8	438	9 HSR01127	HSR01127 H. sapiens r
40	310.2	33.8	372	9 AB063793	AB063793 Homo sapi
41	309.4	33.7	375	9 HSU08102	U08102 Human immun
42	308.8	33.6	529	9 HSU43759	U43759 Human immun
43	308.8	33.6	796	9 AB064130	AB064130 Homo sapi
44	307.8	33.5	375	9 HSA245275	AJ245275 Homo sapi
45	307.8	33.5	375	9 HSA245276	AJ245276 Homo sapi

## ALIGNMENTS

RESULT 1  
AR139128  
LOCUS AR139128 918 bp DNA  
DEFINITION Sequence 13 from patent US 6207153.  
ACCESSION AR139128  
VERSION AR139128.1 GI:14481624  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 918)  
AUTHORS Dan,M.D., Meiti,P.K. and Kaplan,H.A.  
TITLE Antigen Binding fragments that specifically detect cancer cells,  
nucleotides encoding the fragments, and use thereof for the  
prophylaxis and detection of cancers

JOURNAL Patent: US 6207153-A 13 27-MAR-2001;  
 FEATURES Location/Qualifiers  
 source 1..918  
 /organism="unknown"  
 BASE COUNT 213 a 240 c 264 g 201 t  
 ORIGIN

Query Match 100.0%; Score 918; DB 6; Length 918;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-247;  
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCCTATCGCATCGAGTTGCACTGCTGGTTCCGTAACGTT 60  
 DB 1 GAATTCATGAAAAAACCCTATCGCATCGAGTTGCACTGCTGGTTCCGTAACGTT 60  
 QY 61 GGGCAGCCGATATTTGTGTGAGCGAGTCTCCAGGCAACCTGTTTGTCTCCAGGGAA 120  
 DB 61 GGGCAGCCGATATTTGTGTGAGCGAGTCTCCAGGCAACCTGTTTGTCTCCAGGGAA 120  
 QY 121 AGAGCACCCTCTCTCGAGGGCCAGTCAAGAGTTAGTAGCAGTACTAGCTGGTAC 180  
 DB 121 AGAGCACCCTCTCTCTCGAGGGCCAGTCAAGAGTTAGTAGCAGTACTAGCTGGTAC 180  
 QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGCATCCACAGGGCACT 240  
 DB 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGCATCCACAGGGCACT 240  
 QY 241 GGCATGCCAGAGAGTTGAGTGGCACTGGGTCCGGAGAGACTTCACTCCACATCACT 300  
 DB 241 GGCATGCCAGAGAGTTGAGTGGCACTGGGTCCGGAGAGACTTCACTCCACATCACT 300  
 QY 301 AGACTGAGACCTGAAGATTTTGGAGTGTATTACTGTGACAGATAGTAGTACCTGAC 360  
 DB 301 AGACTGAGACCTGAAGATTTTGGAGTGTATTACTGTGACAGATAGTAGTACCTGAC 360  
 QY 361 ACACCTCAGATCACTTTCGCGAGGAGCAAGGTGAGATCAAGAGCTGTGGCTGCA 420  
 DB 361 ACACCTCAGATCACTTTCGCGAGGAGCAAGGTGAGATCAAGAGCTGTGGCTGCA 420  
 QY 421 CCATCTGTCTCTGGCGGTGGCGGTTCCGAGGTGTGTGATCAAGTGGAGTGGCTCCAG 480  
 DB 421 CCATCTGTCTCTGGCGGTGGCGGTTCCGAGGTGTGTGATCAAGTGGAGTGGCTCCAG 480  
 QY 481 GTGCACTGTGTGAGTCTGGGGGAGCGTGTCCAGCTGGAGGCTCCGTAAGCTCTCC 540  
 DB 481 GTGCACTGTGTGAGTCTGGGGGAGCGTGTCCAGCTGGAGGCTCCGTAAGCTCTCC 540  
 QY 541 TGTGAGCCTGTGATTTCCCTTCAGAGCTTTGCTATGCACTGGTCCGCAAGCTCTA 600  
 DB 541 TGTGAGCCTGTGATTTCCCTTCAGAGCTTTGCTATGCACTGGTCCGCAAGCTCTA 600  
 QY 601 GGCAGAGGCTGAGAGTGGGTGGCAAGTTATATCATATGATGAGAGCACTAAATACGCA 660  
 DB 601 GGCAGAGGCTGAGAGTGGGTGGCAAGTTATATCATATGATGAGAGCACTAAATACGCA 660  
 QY 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGCACTTCCAGAGCAAGGATATCTA 720  
 DB 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGCACTTCCAGAGCAAGGATATCTA 720  
 QY 721 AAAATGAACAGCCTGAGAACTGAGACACGCGTGTCTATTACTGTGCGAGATCAGAC 780  
 DB 721 AAAATGAACAGCCTGAGAACTGAGACACGCGTGTCTATTACTGTGCGAGATCAGAC 780  
 QY 781 CTGTTGGGTGATTAAGCACTAATCGGTGTGAGCTGTGGGGCAAGAGGACACGCTC 840  
 DB 781 CTGTTGGGTGATTAAGCACTAATCGGTGTGAGCTGTGGGGCAAGAGGACACGCTC 840  
 QY 841 ACCGCTCTCTCAGATCCGAAACAAAACCTGATCAGGAGAGAGATGTGAACATCACT 900  
 DB 841 ACCGCTCTCTCAGATCCGAAACAAAACCTGATCAGGAGAGAGATGTGAACATCACT 900  
 QY 901 CACCATTAAGTGAAGCTT 918  
 DB 901 CACCATTAAGTGAAGCTT 918

DB 901 CACCATTAAGTGAAGCTT 918

RESULT 2  
 AR139129/c 918 bp DNA linear PAT 16-JUN-2001  
 LOCUS  
 DEFINITION Sequence 15 from patent US 6207153.  
 ACCESSION AR139129  
 VERSION AR139129.1 GI:14481625  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 1 (bases 1 to 918)  
 AUTHORS Dan, M.D., Maiti, P.K. and Kaplan, H.A.  
 TITLE Antigen binding fragments that specifically detect cancer cells, nucleic acids encoding the fragments, and use thereof for the prophylaxis and detection of cancers

JOURNAL Patent: US 6207153-A 13 27-MAR-2001;  
 FEATURES Location/Qualifiers  
 source 1..918  
 /organism="unknown"  
 BASE COUNT 201 a 265 c 239 g 213 t  
 ORIGIN

Query Match 99.8%; Score 916.4; DB 6; Length 918;  
 Best Local Similarity 99.9%; Pred. No. 2.3e-246;  
 Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCCTATCGCATCGAGTTGCACTGCTGGTTCCGTAACGTT 60  
 DB 918 GAATTCATGAAAAAACCCTATCGCATCGAGTTGCACTGCTGGTTCCGTAACGTT 859  
 QY 61 GGGCAGCCGATATTTGTGTGAGCGAGTCTCCAGGCAACCTGTTTGTCTCCAGGGAA 120  
 DB 858 GGGCAGCCGATATTTGTGTGAGCGAGTCTCCAGGCAACCTGTTTGTCTCCAGGGAA 799  
 QY 121 AGAGCACCCTCTCTCGAGGGCCAGTCAAGAGTTAGTAGCAGTACTAGCTGGTAC 180  
 DB 798 AGAGCACCCTCTCTCTCGAGGGCCAGTCAAGAGTTAGTAGCAGTACTAGCTGGTAC 739  
 QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGTGATCCACAGGGCACT 240  
 DB 728 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGTGATCCACAGGGCACT 679  
 QY 241 GGCATGCCAGAGAGTTGAGTGGCACTGGGTCCGGAGAGACTTCACTCCACATCACT 300  
 DB 678 GGCATGCCAGAGAGTTGAGTGGCACTGGGTCCGGAGAGACTTCACTCCACATCACT 619  
 QY 301 AGACTGAGACCTGAAGATTTTGGAGTGTATTACTGTGACAGATAGTAGTACCTGAC 360  
 DB 618 AGACTGAGACCTGAAGATTTTGGAGTGTATTACTGTGACAGATAGTAGTACCTGAC 559  
 QY 361 ACACCTCAGATCACTTTCGCGAGGAGCAAGGTGAGATCAAGAGCTGTGGCTGCA 420  
 DB 558 ACACCTCAGATCACTTTCGCGAGGAGCAAGGTGAGATCAAGAGCTGTGGCTGCA 499  
 QY 421 CCATCTGTCTCTGGCGGTGGCGGTTCCGAGGTGTGTGATCAAGTGGAGTGGCTCCAG 480  
 DB 498 CCATCTGTCTCTGGCGGTGGCGGTTCCGAGGTGTGTGATCAAGTGGAGTGGCTCCAG 439  
 QY 481 GTGCACTGTGTGAGTCTGGGGGAGCGTGTCCAGCTGGGAGGCTCCGTAAGCTCTCC 540  
 DB 438 GTGCACTGTGTGAGTCTGGGGGAGCGTGTCCAGCTGGGAGGCTCCGTAAGCTCTCC 379  
 QY 541 TGTGAGCCTGTGATTTCCCTTCAGAGCTTTGCTATGCACTGGTCCGCAAGCTCTA 600  
 DB 378 TGTGAGCCTGTGATTTCCCTTCAGAGCTTTGCTATGCACTGGTCCGCAAGCTCTA 319  
 QY 601 GGCAGAGGCTGAGAGTGGGTGGCAAGTTATATCATATGATGAGAGCACTAAATACGCA 660  
 DB 318 GGCAGAGGCTGAGAGTGGGTGGCAAGTTATATCATATGATGAGAGCACTAAATACGCA 259

QY 661 GACTCCGTGAAGGCGCATTCACCATCTCCAGAGACACTTCCAGAAACCGGTATCTTA 720  
 Db 258 GACTCCGTGAAGGCGCATTCACCATCTCCAGAGACACTTCCAGAAACCGGTATCTTA 199  
 QY 721 AAATGAACAGCCCTGAGAACCTGAGACACCGCTGTCTTATTACTGTGGAGAGATCAGAGC 780  
 Db 198 AAATGAACAGCCCTGAGAACCTGAGACACCGCTGTCTTATTACTGTGGAGAGATCAGAGC 139  
 QY 781 CTGTGGGTGACTATGACCACTACTACGTTTGAACGCTGTGGGCAAGGAGACACGCTC 840  
 Db 138 CTGTGGGTGACTATGACCACTACTACGTTTGAACGCTGTGGGCAAGGAGACACGCTC 79  
 QY 841 ACCGTCTCTTCAGAGATCCGAACAAAACCTGATCAGCGAAGAAATCTGAACCATCACCAT 900  
 Db 78 ACCGTCTCTTCAGAGATCCGAACAAAACCTGATCAGCGAAGAAATCTGAACCATCACCAT 19  
 QY 901 CACCATTAATGGAAGCTT 918  
 Db 18 CACCATTAATGGAAGCTT 1

## RESULT 3

AR139130 AR139130 867 bp DNA linear PAT 16-JUN-2001  
 LOCUS Definition Sequence 16 from patent US 6207153.  
 ACCESSION AR139130  
 VERSION AR139130.1 GI:14481626  
 KEYWORDS

## SOURCE

ORGANISM Unknown.  
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 867)  
 AUTHORS Dan, M.D., Maiti, P.K. and Kaplan, H.A.  
 TITLE Antigen binding fragments that specifically detect cancer cells,  
 nucleotides encoding the fragments, and use thereof for the  
 prophylaxis and detection of cancers  
 Patent: US 6207153-A 16 27-MAR-2001;  
 Location/Qualifiers

JOURNAL  
 FEATURES  
 source 1..867  
 /organism="unknown"

BASE COUNT 209 a 229 c 241 g 188 t

ORIGIN

Query Match 87.1%; Score 799.6; DB 6; Length 867;  
 Best Local Similarity 94.0%; Pred. No. 1.6e-213;  
 Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

QY 1 GAATTCATGAAAAAACCGCTATCGCATGCGAGTTGCACTGGCTGTTGCTACCGTT 60  
 Db 1 GAATTCATGAAAAAACCGCTATCGCATGCGAGTTGCACTGGCTGTTGCTACCGTT 60  
 QY 61 GCGGAGGCCCATATTGTTGTTAAGCAGTCCTCCAGGACCCCTGTTGTCTCCAGGGAA 120  
 Db 61 GCGGAGGCCCATATTGTTGTTAAGCAGTCCTCCAGGACCCCTGTTGTCTCCAGGGAA 120  
 QY 121 AGAGCCACCCCTCTCTGAGGGGAGTCAGAGTGTATTAGACAGTACTTGAAGCTGTATC 180  
 Db 121 AGAGCCACCCCTCTCTGAGGGGAGTCAGAGTGTATTAGACAGTACTTGAAGCTGTATC 180  
 QY 181 CAGGAGAAACCTGCGCAGAGCTCCAGAGCTCTCACTATGATGATCCACAGGAGCACT 240  
 Db 181 CAGGAGAAACCTGCGCAGAGCTCCAGAGCTCTCACTATGATGATCCACAGGAGCACT 240  
 QY 241 GGCATGCGCAGCAGATTCAGTGGGAGTGGGTCCGGGAGAACTTCACTCTCAACATCAGT 300  
 Db 241 GGCATGCGCAGCAGATTCAGTGGGAGTGGGTCCGGGAGAACTTCACTCTCAACATCAGT 300  
 QY 301 AGACTGAGCCTGAAGATTTTGCAGTGTATTACTGTCAAGATAGTATGAGTCAACCTGAG 360  
 Db 301 AGACTGAGCCTGAAGATTTTGCAGTGTATTACTGTCAAGATAGTATGAGTCAACCTGAG 360  
 QY 361 ACACCTCAGATCACTTTGCGGCGAGAGGACCAAGGTGAGATCAACGAATGTGGCTGCA 420

Db 361 ACACCTCAGATCACTTTGCGGCGAGAGGACCAAGGTGAGATCAACGAATGTGGCTGCA 420  
 QY 421 CCAATCTCTCTGCGCGGTGGCGGTTCCGAGGTGTGATCAGGTGAGGTGCCCTCCAG 480  
 Db 421 TC-----CGACAG 429  
 QY 481 GTGAGCTGTGTGAGTCTGCGGGAGGCGGTGTCCAGCTTGGAGAGTCCCTGAGACTCTCC 540  
 Db 430 GTGAGCTGTGTGAGTCTGCGGGAGGCGGTGTCCAGCTTGGAGAGTCCCTGAGACTCTCC 489  
 QY 541 TGTGCAACCTCTGATATCCCTTCCAGAAAGCTTTGCTATGACATGAGTCCCGCAGAGCTTA 600  
 Db 490 TGTGCAACCTCTGATATCCCTTCCAGAAAGCTTTGCTATGACATGAGTCCCGCAGAGCTTA 549  
 QY 601 GGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAACACTTAATTAATCAAGCA 660  
 Db 550 GGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAACACTTAATTAATCAAGCA 609  
 QY 661 GACTCCGTGAAGGCGCATTCACCATCTCCAGAGACACTTCCAGAAACCGGTATCTTA 720  
 Db 610 GACTCCGTGAAGGCGCATTCACCATCTCCAGAGACACTTCCAGAAACCGGTATCTTA 669  
 QY 721 AAATGAACAGCCCTGAGAACCTGAGACACCGCTGTCTTATTACTGTGGAGAGATCAGAGC 780  
 Db 670 AAATGAACAGCCCTGAGAACCTGAGACACCGCTGTCTTATTACTGTGGAGAGATCAGAGC 729  
 QY 781 CTGTGGGTGACTATGACCACTACTACGTTTGAACGCTGTGGGCAAGGAGACACGCTC 840  
 Db 730 CTGTGGGTGACTATGACCACTACTACGTTTGAACGCTGTGGGCAAGGAGACACGCTC 789  
 QY 841 ACCGTCTCTTCAGAGATCCGAACAAAACCTGATCAGCGAAGAAATCTGAACCATCACCAT 900  
 Db 790 ACCGTCTCTTCAGAGATCCGAACAAAACCTGATCAGCGAAGAAATCTGAACCATCACCAT 849  
 QY 901 CACCATTAATGGAAGCTT 918  
 Db 850 CACCATTAATGGAAGCTT 867

## RESULT 4

AR139131/c AR139131 867 bp DNA linear PAT 16-JUN-2001  
 LOCUS Definition Sequence 18 from patent US 6207153.  
 ACCESSION AR139131  
 VERSION AR139131.1 GI:14481627  
 KEYWORDS

## SOURCE

ORGANISM Unknown.  
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 867)  
 AUTHORS Dan, M.D., Maiti, P.K. and Kaplan, H.A.  
 TITLE Antigen binding fragments that specifically detect cancer cells,  
 nucleotides encoding the fragments, and use thereof for the  
 prophylaxis and detection of cancers  
 Patent: US 6207153-A 18 27-MAR-2001;  
 Location/Qualifiers

JOURNAL  
 FEATURES  
 source 1..867  
 /organism="unknown"

BASE COUNT 189 a 241 c 229 g 208 t

## ORIGIN

Query Match 86.9%; Score 798; DB 6; Length 867;  
 Best Local Similarity 93.9%; Pred. No. 4.6e-213;  
 Matches 862; Conservative 0; Mismatches 5; Indels 51; Gaps 1;

QY 1 GAATTCATGAAAAAACCGCTATCGCATGCGAGTTGCACTGGCTGTTGCTACCGTT 60  
 Db 867 GAATTCATGAAAAAACCGCTATCGCATGCGAGTTGCACTGGCTGTTGCTACCGTT 808  
 QY 61 GCGGAGGCCCATATTGTTGTTAAGCAGTCCTCCAGGACCCCTGTTGTCTCCAGGGAA 120  
 Db 807 GCGGAGGCCCATATTGTTGTTAAGCAGTCCTCCAGGACCCCTGTTGTCTCCAGGGAA 748

QY	121	AGAGCACCCCTCTCTCGAGGGGCCAGTCAGAGTGTATAGACAGTACTTGACCTGGAC	180
Db	747	AGAGCACCCCTCTCTCTCGAGGGCCAGTCAGAGTGTATAGACAGTACTTGACCTGGAC	688
QY	181	CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGTGTGATCCACAGGGCCACT	240
Db	687	CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGTGTGATCCACAGGGCCACT	628
QY	241	GGCATGCCAGACAGGTTCAGTGGCAGTGGGTCCGGACAGACTTCACTCTCAACATCAGT	300
Db	627	GGCATGCCAGACAGGTTCAGTGGCAGTGGGTCCGGACAGACTTCACTCTCAACATCAGT	568
QY	301	AGACTGGAGCCTGAAAGATTTTGACAGTGTATTACTGTCAAGCAGTATGTAGTCACTCCAG	360
Db	567	AGACTGGAGCCTGAAAGATTTTGACAGTGTATTACTGTCAAGCAGTATGTAGTCACTCCAG	508
QY	361	ACACCTCAGATCACTTTCGGCGAGGGACCAAGGTGAGATCAACAGAACTGTGGCTGCA	420
Db	507	ACACCTCAGATCACTTTCGGCGAGGGACCAAGGTGAGATCAACAGAACTGTGGCTGCA	448
QY	421	CCATCTGTCTCTGGCGGTGCGGTTCCGAGGTGATGATAGGTGAGGTGCTCCAG	480
Db	447	TC-----CGACAG 439	
QY	481	GTGACAGCTGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGAGGTCCTGAGACTGCC	540
Db	438	GTGACAGCTGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGAGGTCCTGAGACTGCC	379
QY	541	TGTGCAGCCTCTGAGATTCCCTTCAGAAAGCTTTCGATATGCACTGGGTCGGCAGGCTCTA	600
Db	378	TGTGCAGCCTCTGAGATTCCCTTCAGAAAGCTTTCGATATGCACTGGGTCGGCAGGCTCTA	319
QY	601	GGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGCATTAATATCTACGCA	660
Db	318	GGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGCATTAATATCTACGCA	259
QY	661	GACTCCGGAAGGGCCGAAATTCACATCTCCAGAGCAGCTTCCAGAAACAGGGTGAATCTA	720
Db	258	GACTCCGGAAGGGCCGAAATTCACATCTCCAGAGCAGCTTCCAGAAACAGGGTGAATCTA	199
QY	721	AAAAATGAACAGCCTGAGAGATGAGAGCAGCGCTGTCTATTACTGTGCGAGAGATCAGAGC	780
Db	198	AAAAATGAACAGCCTGAGAGATGAGAGCAGCGCTGTCTATTACTGTGCGAGAGATCAGAGC	139
QY	781	CTGTTGGGTGACTATGACCACTACTACGAGTTTGAAGTCTGGGGCAAAAGGACCAAGGTC	840
Db	138	CTGTTGGGTGACTATGACCACTACTACGAGTTTGAAGTCTGGGGCAAAAGGACCAAGGTC	79
QY	841	ACCGTCTCTCAGAGTCCGGAACAAAACCTGATCAGCGAAGAAAGATCTAAACATACAT	900
Db	78	ACCGTCTCTCAGAGTCCGGAACAAAACCTGATCAGCGAAGAAAGATCTAAACATACAT	19
QY	901	CACCATTAGTGAAGCTT 918	
Db	18	CACCATTAGTGAAGCTT 1	
RESULT 5			
AF027160		801 bp mRNA linear SYN 06-FEB-2003	
LOCUS			
DEFINITION		Synthetic construct single chain Fv fragment (76JscFv07) mRNA,	
ACCESSION		AF027160	
VERSION		AF027160.2 GI:23683339	
KEYWORDS			
SOURCE		synthetic construct	
ORGANISM		synthetic construct	
REFERENCE		artificial sequences.	
AUTHORS		1 (bases 1 to 801)	
TITLE		Ohba,H., Kashima,K., Tomozawa,T. and Chiba,J.	
		Molecular expression of human antibody and prediction of	
		antigen-binding structure	
		(IM)PROCEEDINGS OF THE JAPANESE SOCIETY OF IMMUNOLOGY: 639;	

REFERENCE	2 (bases 1 to 801)
AUTHORS	Ohba,H., Kaashima,K., Tomozawa,T. and Chiba,J.
TITLE	Direct Submission
JOURNAL	Submitted (29-SEP-1997) Department of Biological Sciences and Technology, Science University of Tokyo, 2641 Yamazaki, Noda, Chiba 278, Japan
REFERENCE	3 (bases 1 to 801)
AUTHORS	Ohba,H., Kaashima,K., Tomozawa,T. and Chiba,J.
TITLE	Direct Submission
JOURNAL	Submitted (10-OCT-2002) Department of Biological Sciences and Technology, Science University of Tokyo, 2641 Yamazaki, Noda, Chiba 278, Japan
REMARK	Sequence update by submitter
COMMENT	On Oct 10, 2002 this sequence version replaced gi:2623588.
FEATURES	Location/Qualifiers

```

source
1. .801
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/clone="TAPC6JC5"
/note="TAPC6JC5 hybridoma was made by fusing an EBV transformed B cell line, TAPC01-C14 with triple hybridoma, 6JC5; sequence based on human DNA"
1. .801
/gene="T6USCFV07"
1. .801
CDS
1. .801

```

```

/note="specific to hepatitis B virus surface antigen"
/codon_start=1
/transl_table=11
/product="single chain Fv fragment"
/protein_id="AAB86468.2"
/db_xref="GI:23683340"
/translation="METHPAQLFLLILMLPVSDTGTIWMQSPATISVSPGERATIS
CRASQSVRNILAWYQKRPQAPRLIIYAASRAIGIIPARSGSGTEFLTITISLQS
EDPFIYVYCOOINWFPTFGQGTIKVEIKSRGGSGGGSGGGLQLEQVLAESGCGVIV
QPGSLSLCYASGETPSSSYPMNTVRAQPGKLEWVASISDGSYKKYKVDSEMKRLRTI
SRDSKNTLIYEMNSLTAEDTAVYYCARLAFNNAIVDWGGQITLVTS"

```

```

sig_peptide      1. .66
                  /gene="TeJuscFv07"
mat_peptide      67. .387
                  /gene="TeJuscFv07"
                  /product="light chain Fv fragment"
mat_peptide      445. .798
                  /gene="TeJuscFv07"
                  /product="heavy chain Fv fragment"
misc_feature      386. .444
                  /gene="TeJuscFv07"

```

```

/notes="encodes flexible linker peptide"
BASE COUNT 181 a 212 c 229 g 179 t

```

Query Match	50.5%	Score 463.8;	DB 12;	Length 801;
Best Local Similarity	82.3%;	Pred. No. 4:2e-119;		
Matches 592; Conservative	0;	Mismatches 97;	Indels 30;	Gaps 4;

QY	52	GCTACCGTTGGCGACGCCGATATTGTGTAGAGAGTCTCCAGGACCCCTGCTTGGCT	111
Db	49	GTTTCAGATACCTCGAGAAATGATGTAGCGAGTCTCCAGCACCTCTGTCTGTCT	108
QY	112	CCAGGGGAAAGAGCCACCTCTCTCTGCGAGGCGCAGTCAAGTGTATGAGCAGCTACTTA	171
Db	109	CCAGGGGAAAGAGCCACCTCTCTCTGCGAGGCGCAGTCAAGATGTTAGAAGC---ACTTA	165
QY	172	GCTTGATCCAGCAGAAACCTTGCCAGGCTCCAGGCTCTTCATCTATGTGTGATCCACC	231
Db	166	GCTTGATCCAGCAGAAACCTTGCCAGGCTCCAGGCTCTTCATCTATGTGTGATCCACC	225
QY	232	AGGCGCATGTGCATCCGACAGAGTTCAAGTGTGGCTCCGGACAGACTTCATCTCTC	291
Db	226	AGGCGCATGTGTATCCGACAGGTTCAAGTGTGGCTCTGGACAGAGTTCACTCTC	285

Query	March	48.5%;	Score 445;	DB 6;	Length 1630;	
Best	Local	Similarity	76.3%;	Prod. No. 8.2e-14;		
Matches	620;	Conservative	0;	Mismatches 145;	Indels 48;	Gaps 4

  

QY	52	GCTACCGTGGGACAGGCCGATATTGTGTGACGAGTCTCCAGGACCCCTGTCCTT	111
DB	78	GCTACAGGTGACACTCCGAGCTCCAGATGACCAGTCCATCTCTCCTGTCTGATCT	137
QY	112	CCAGGGGAAAGACACCCCTCTCCTGCAGGGCCAGTCAGTGTATTAGACAGCTACTTA	171
DB	138	GTAGAGAGCAGAGTCACCATCATCTTGGCGGCAAGTCAGAG---CATTAGCAGCTATTTA	194
QY	172	GCTGTGTACCAAGCAAAACCTGGCCAGGCTCCAGGCTCTCTCATTTATGTGTGATCCAC	231
DB	195	AATTGTGTATCGACGAAACCAAGACAGGCTCTTAAGCTGTCTATTACTGTGGCATCTACC	254
QY	232	AGGGCCACTGSCATATGCCAGAGGTTACGTGGCAGTGGTCCGGGACAGACTTACCTTC	291
DB	255	CGGGAATCCGGGGTCCCTCGACCGATTACGCGGCAGTGATCTGGGACAAATTCACCTTC	314
QY	292	ACCATCATGTAAGTCTGAGCCTGGAAGATTTTGCAGTGTATCTGTACAGATGTGTAGC	351
DB	315	ACCATTCAGACCTGTGACGCTGAAAGATTTCCTACTTACTTTTGTTCACACGTCTACAGT	374
QY	352	TCACTTAGACACCTCATGATCATCTTTCGCGGAGAGGACCAAGTGTGATCAAAAGAACT	411
DB	375	TTTGGC-----GATCATCTTGGGCAAGGACACGACTGTGACATTTCA-----	416
QY	412	GTGGCTGACCATCTGTCTCTGGCGGCTGGCGGTTCCGAGGTGTGTGATCAGGTGTGAGGT	471

Df		458	GGCATCAGAGGATGGACCTGCTCGAGTCTGGGGAAGCCGTGGTCACGCCCTGGGAGGCTCCG	513
Oy		532	AGACTCTCTGTGCAAGCCTCTGATATTCCCTTCAGAAGCTTTGCTATGCACTGGGTCGCG	591
Dd		516	AGACTCTCTGTGCAAGCCTCTGATATTCCCTTCAGAAGCTTTGCTATGCACTGGGTCGCG	575
Oy		592	CAGCCTTAGGCAGAGGGCTGAGTGAGTGGTGCAATTATCATATGATGAGAACCTAA	651
Dd		576	CAGCCTCAGGCAGAAAGGGCTGAGTGGTGCAATTATCATATGATGAGAACCTAA	635
Oy		652	TACTAAGCAGCTCCGTGAAAGGGCCGATTACCAATCTCAGAGACACTTCCAAGAACG	711
Dd		636	TACTATGAGACTCCGTGAAAGGGCCGATTACCAATCTCAGAGACAAATTCGAAGAACG	695
Oy		712	GTCATATCTAAATAATGAAACAGCCTGAGACTAGAGACAAGCGCTGTCTATTATCTGTSCGAGA	771
Dd		696	CTGTATCTGCAGAAATGAAACAGCCTGAGACTAGAGACAAGCGCTGTCTATTATCTGTSCGAAA	755
Oy		772	GATCAGAGACCTGTTGGGTGACT-----ATGACCATACTACGAGTTTGGACGCTGGGGC	825
Dd		756	GATATGGGGGTGGGACAGTGGCTGAGACCTTACTACTACGATAGGATGACGTCGGGGC	815
Oy		826	AAAGGACCAACGGTCACCGCTCTCTCTCAGGAATCC	858
Dd		816	CAAAGGACCAACGGTCACCGCTCTCTCTCAGGAATCC	848

RESULT 7  
AX023367

LOCUS	AX023367	1630 bp	DNA	linear	PAT 15-SEP-2000
DEFINITION	Sequence 38 from Patent WO0006605.				
ACCESSION	AX023367				
VERSION	AX023367.1 GI:10183779				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				

REFERENCE 1  
 AUTHORS Kufer, P., Zetli, F., Dreier, T., Baerle, P. A. and Borschert, K.  
 TITLE Heteromibodies  
 JOURNAL Patent: WO 0006605-A 38 10-FEB-2000;  
 KUPER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;  
 BAERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GBS FUER  
 BIOMEDIZINIS (DE)  
 FEATURES  
 source  
 1. .1630  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 39. .1613  
 /note="unnamed protein product"  
 /codon\_start=1  
 /protein\_id="CAC08836.1"  
 /db\_xref="GI:10183780"  
 /translation="MGMSCTILFLVATATGVSLEQMTQSPSSLSASVGRDVTTCRA  
 SOSISYLMWYQKPGQPKLITVMASTBESGVPDPFSGSEGTNYLTISLOPEDF  
 ATYFCQSDSLPTTFGQTRLDIOGGGGGGGGGGSEVOLLESGGVVQGRSLR  
 LSCASGTFSSYGMHWROAPBKGLEWYAVISYDSNRYADSVYGRFTISRDNSKN  
 TLYLQNSLRARDEPTAVYCAKMGSSGMRPYITVMDVWGQGTITVSSGPLEGDT  
 HRTVAASVFIPEPDEQKSGTASVCLNNFYPRANKVQKVNALQSDSV  
 TEODSKDSTYSLSSTLTLSKADYERKAVACEVTHQSLSPVTKSPNRCGCGGSA  
 PTSSSTKTKTQLQLEHLIDLOMLINGINNYKPKLRLMLTFPKYMKKATELKHQL  
 EEELKLEEVNLAOSKNFHLRPRDLISINIVYIELKSGSETTFCVEADETATVEF  
 LNRWTFQCSIIISLT"  
 BASE COUNT 445 a 410 c 408 g 367 t  
 ORIGIN  
 Query Match 48.5%; Score 445; DB 6; Length 1630;  
 Best Local Similarity 76.3%; Pred. No. 8.2e-114;  
 Matches 620; Conservative 0; Mismatches 145; Indels 48; Gaps 4;

QY 652 TACTACGAGACTCCGTGAAAGGCGCATTCACCATCTCCAGAGACCTTCAAGACAG 711  
 |||||  
 DB 636 TACTATGAGACTCCGTGAAAGGCGCATTCACCATCTCCAGAGACCTTCAAGACAG 695  
 |||||  
 QY 712 GTGATCTTAAAAATGAACAGCTGAGAACTGAGACACAGCGTGTCTATTACTGTGAG 771  
 |||||  
 DB 696 CTGTATCTTCAATGAACAGCTGAGAGCTGAGACACAGCGTGTCTATTACTGTGAG 755  
 |||||  
 QY 772 GATCAGAGCTGTGGGTGACT-----ATGACCACTACTAGCTTTGACGCTCGGGC 825  
 |||||  
 DB 756 GATATGGGGTGGGAGAGGTGAGACCTTACTACTACTAGTATGAGACGCTCGGGC 815  
 |||||  
 QY 826 AAAGGACCAAGCTGACCGTCTCTCAGAGATCC 858  
 |||||  
 DB 816 CAAGGACCAAGCTGACCGTCTCTCAGAGATCC 848  
 |||||  
 RESULT 8  
 AF416910  
 LOCUS  
 DEFINITION Synthetic construct JB-43 recombinant single chain Fv antibody  
 derivative mRNA, partial cds.  
 ACCESSION AF416910  
 VERSION AF416910.1 GI:16033614  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 synthetic construct  
 artificial sequences.  
 1 (bases 1 to 867)  
 Bangle, Y., Li, L., Cavalli, D., Gordon, T., Karle, S., Planque, S.,  
 Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and  
 Paul, S.  
 Broad distribution and disease association of vasoactive intestinal  
 peptide binding and cleaving autoantibodies  
 2 (bases 1 to 867)  
 Bangle, Y., Li, L., Cavalli, D., Gordon, T., Karle, S., Planque, S.,  
 Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and  
 Paul, S.  
 Direct Submission  
 Submitted (06-SEP-2001) Pathology and Laboratory Medicine,  
 University of Texas-Houston Medical School, 6431 Fannin, Houston,  
 TX 77030, USA  
 FEATURES  
 source  
 location/Qualifiers  
 1. .867  
 /organism="synthetic construct"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:32630"  
 /focus  
 1. .786  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="JB-43"  
 /cell\_type="PB; B-lymphocyte"  
 /dev\_stage="adult"  
 /note="selected from lupus phage library on Bt-VIP"  
 <1. .867  
 /codon\_start=1  
 /transl\_table=11  
 /product="recombinant single chain Fv antibody derivative"  
 /protein\_id="AA113299.1"  
 /db\_xref="GI:16033615"  
 /translation="EIVLTQSPGTLISLSPGERATISCPASQSVRSDDLAMTQKFGQA  
 PRLIYASPRATGIPDRFSGSGSGSGLAQVQLQSGPGLVPSRSLSLCTVSGSVSSGS  
 GTYDIKRSAGGSGSGSGLAQVQLQSGPGLVPSRSLSLCTVSGSVSSGS  
 YVMSWIRPAGKGLMIGRIYTSSTINYPILSKSVITISVPSKNOFSLKLSVTAA  
 TAVYCAVAGSGWGYGYYGMDVWGQGTITVSSGSASAPTLFPAALHHHHHGAEO  
 KLISEEDLNGAA"  
 796. .813  
 /note="Region: poly-histidine tag"  
 823. .855  
 misc\_feature  
 misc\_feature

V_region	/note="Region: c-myc tag"
	<1. .330
misc_feature	/note="light chain variable domain"
	331..378
V_region	/note="linker between VL and VH domains"
	379..786
	/note="heavy chain variable domain"
BASE COUNT	183 a 251 c 179 t
ORIGIN	

Query Match	45.1%;	Score 414.4;	DB 12;	Length 867;
Best Local Similarity	73.9%;	Pred. No. 3.3e-105;		
Matches 625;	Conservative 0;	Mismatches 176;	Indels 45;	Gaps 6

OY	70	GATATTTGGTTACGAGCTCTCAGGACCCCTGTCTTTGGTCTCAGGGGAAAGACACC	129
Db	1	GAATTTGGTTACGAGCTCTCAGGACCCCTGTCTTTGGTCTCAGGGGAAAGACACC	60
OY	130	CTCTCTCTGACGGGCCAGTCAAGTGTTTAGTAGCAGCTACTTAACTGAGTACGACGAAA	189
Db	61	CTCTCTCTGACGGGCCAGTCAAGTGTTTAGTAGCAGCAGCTTAACTGAGTACGACGAAA	120
OY	190	CTTGGCCAGGGCTTCCAGGCTCCTCACTATATGGTGAATCCACAGGGGCCACTGGCAATGCCA	249
Db	121	CTTGGCCAGGGCTTCCAGGCTCCTCACTATATGGTGAATCCAGGAGGGCCACTGGCAATGCCA	180
OY	250	GACAGGTTCAGTGGCAGTGGGTCCGGGACAGACTTCACTCTCAACATCACTAGTACCTGGAG	309
Db	181	GACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCAACATCACTAGTACCTGGAG	240
OY	310	CCTGAAGAATTTTGGCACTGTATTAATCTCAGCAGATATGATAGTCACTCACTAGAACCTTCAG	369
Db	241	CCTGAAGAATTTTGGCACTGTATTAATCTCAGCAGTATGATAGTCACTCACTAGTAACTTCAG	291
OY	370	ATCATCTTTGGCGGAGGGGACCAAGGTGGAGATCAACAGAACTGTGGCTGACCATCTGTCTC	429
Db	292	TTCACTTTTGGCGCTGTGGACCAAAAGTGAATTCAAACGCTC-----G	333
OY	430	TCTGCGGTGGCGGTTCCGGAAGTGTGATATCAGGTGAAGGTGGCTCCAGGTGCAGCTG	489
Db	334	AGTGTGTGAGGGGGTTCAGGCGGAGGTGTGCTGGGGGTAGTGACATTCAGGTGCAGCTG	393
OY	490	GTGAGGTCTGAGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCTGTGACAGCC	549
Db	394	CAGGAGTGGGGGCCAGGACTGTGGAGACCTTCCGAGAACCTGTGCTCTCACTTCACTGATCTC	453
OY	550	TCTGGAATTCCTTCAGAACTTGTCT-----ATGCACTGGGTCCGCCAGGCTCTAAGGC	603
Db	454	TCTGATGGCTCCGTCAGTATGTGGTAGTATCTACTGAGGCTGGAATCCGGGACGCCGCCGGG	513
OY	604	AAAGGGCTTGGATTTGGGTGCACTTATATCATATGATGGAAGACCTTAATCTACGACGAC	663
Db	514	AAAGGACTTGGATTTGGGCGTATCTTATACCAAGTGGAGGACCAACTAACACCCG---	570
OY	664	TCCGTGAAGGGCCGATTCAACACTCTCCAGAGCACTTCCAGAAACACGGGTATCTTAATA	723
Db	571	TCCCTTCAGAGTGCAGTACATATATAGTAGACACGTCCAAAGAACAGTTCCTCCCTGAAG	630
OY	724	ATGAACAGCTTGAAGAACTGAGAGCACGGCTGTCTATTACTGTGCGAGAGATCAAGCCTG	783
Db	631	CTGAGCTCTGTACACCGCCGACAGACGGCCGTGTACTACTGTGCGAGAGTGTGCACTGTGC	690
OY	784	TTGGGTGACTATGACACACTACTACGGTTTGGAGGTCTGGGGGCAAAAGGAGCAGGGTCAAC	843
Db	691	T---GGTACGGTGTACTACTACGGTATGAGAGTCTGGGGGCCAAAGGAGCAGGGTCAAC	747
OY	844	GTCTCTCTCAG-----ATCCGAACAAAACTGATCAGCGAGAGAAGATCTGAACATCAC	897
Db	748	GTCTCTCTCAGGAGTGCATCTCCGCCAACCTTTTCCCGCGGCCGACATCATCATCAC	807
OY	898	CATCAC	903
Db	808	CATCAC	813

RESULT 9	
LOCUS AF416909	861 bp mRNA linear SYN 11-OCT-2001
DEFINITION Synthetic construct JB-14 recombinant single chain Fv antibody derivative mRNA, partial cds.	
ACCESSION AF416909	
VERSION AF416909.1 GI:16033611	
KEYWORDS synthetic construct synthetic construct artificial sequences. 1 (bases 1 to 861) Bangale,Y., Li,L., Cavall,D., Gordon,T., Karle,S., Pianque,S., Zhou Y.-X., Taguchi,H., Bhatia,G., Nishiyama,Y., Arnett,F. and Paul,S. Broad distribution and disease association of vasoactive intestinal peptide binding and cleaving autoantibodies	
TITLE JOURNAL REFERENCE AUTHORS	
JOURNAL REFERENCE AUTHORS	
2 (bases 1 to 861)	
Bangale,Y., Li,L., Cavall,D., Gordon,T., Karle,S., Pianque,S., Zhou Y.-X., Taguchi,H., Bhatia,G., Nishiyama,Y., Arnett,F. and Paul,S.	
Direct Submission Submitted (06-SEP-2001) Pathology and Laboratory Medicine, University of Texas-Houston Medical School, 6431 Fannin, Houston, TX 77030, USA	
FEATURES SOURCE	
location/Qualifiers	
1..861 /organism="Synthetic construct"	
/mol_type="mRNA"	
/db_xref="taxon:32630"	
/focus	
1..780 /organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="UB-14"	
/cell_type="PBL; B-Lymphocyte"	
/dev_stage="adult"	
/note="Selected from lupus phage library on Bc-VIP"	
<1..861 /codon_start=1	
/transl_table=1	
/product="recombinant single chain Fv antibody derivative"	
/protein_id="AAU13298.1"	
/db_xref="GI:16033612"	
/translation="ETLTQSPATLSLSPERATISCRASQSVSYLAHWYQOKPGOAPRLIHRDSNRATGPARFSGSSGGSDPTLRILSLPEDPFAVYYCCGSNDMDFGGGT KLRIKRSRSGSGSGSGSSALAQVOQAQGSRPLRYKRSGTSLCTYSGSISSYYWGMGRHPHGKLENTGITTVTSSTNPSLKSRVTISVDTSKNQSF.LKSIVRADTR ISEEDLNAGAA"	
790..807 /note="Region: poly-histidine tag"	
817..849 /note="Region: C-myc tag"	
<1..324 /note="light chain variable domain"	
325..372 /note="linker between VL and VH domains"	
373..780 /note="heavy chain variable domain"	
BASE COUNT 191 a 258 c 241 g 171 e	
ORIGIN	
Query Match 40.3%; Score 369.6; DB 12; Length 861;	
Best Local Similarity 71.9%; Pred.No.1.3e-92;	
Matches 601; Conservative 0; Mismatched 184; Indels Gaps 7;	
80 TGACGCAGTCGCCAGCACCTGTTTGTTGTTCCAGGGGAAGCACCCTTCCTCA 139	

Db 11 TCACGAGTCTCCAGCACCCCTGTCTTGTCTCCAGGGAAAGGACCCCTCTCCGCA 70  
 QY 140 GGGCCAGTCAAGTGTAGTACGACTTACTTGTGTACGAGCAAAACCTGGCCAG 199  
 Db 71 GGGCCAGTCAAGTGT---TAGCAGTCACTTACCTGTGTACCAAGAAACCTGGCCAG 127  
 QY 200 CTCGCCAGGCTCTCATCTATGTGATCCACAGGGCCATGTGATGCGAGAGGTCA 259  
 Db 128 CTCGCCAGGCTCTCATCTATGTGATCCACAGGGCCATGTGATGCGAGAGGTCA 187  
 QY 260 GTGGCAGTGGTCCGGACAGACTTCACTCTCACTCACTAGTACCTGGAGGATT 319  
 Db 188 GTGGCAGTGGTCCGGACAGACTTCACTCTCACTCACTAGTACCTGGAGGATT 247  
 QY 320 TTGCAAGTATTACTGTGACAGTATGTGTACCTCAGACCTCAGATACCTTGG 379  
 Db 248 TTGCAAGTATTACTGTGACAGTATGTGTACCTCAGACCTCAGATACCTTGG 295  
 QY 380 GCGAGAGGACCAAGTGAAGATCAAGAACTGTGGCTGACCATCTGTCTTGGCGTG 439  
 Db 296 GCGAGAGGACCAAGTGAAGATCAAGAACTGTGGCTGACCATCTGTCTTGGCGTG 337  
 QY 440 GCGGTTCCGAGGTGTGATCAGTGAAGTGGCTCCAGTGAAGTGTGAGTGTG 499  
 Db 338 GCGGTTCCGAGGTGTGATCAGTGAAGTGGCTCCAGTGAAGTGTGAGTGTG 397  
 QY 500 GGGGAGCGGTGTGACAGCTGGAGGCTCCAGTGTCTGTGAGCTCTGTGATTC 559  
 Db 398 GCGCAAGACTGTGAAGCTTCGGGAGCCCTGTCTCACTGCTGTCTGTGAGTTC 457  
 QY 560 CCTTCAGAACTTGTCTATGCACTGGG-----TCCGCGAGGCTTGAAGGAGGCTGG 613  
 Db 458 CCATCAGAGTGTAGTACTTACTGTGGGGCTGATCCGCCAGCAGCCAGGGAAGGCTGG 517  
 QY 614 AGTGGGTGCACTTATATCATATGATGAAGCACTAAATCTAGCAGACTCCGTGAAG 673  
 Db 518 AGTGAATTTGGTATCATCTATTAATGAGGAGCACTTATCAACACC---GTCCCTCAGA 574  
 QY 674 GCGATTCACCATCTCCAGAGCACTTCCAGAAACAGCGGTATCTAAATGAAGACGCC 733  
 Db 575 GTGAGTCAACCATATCATATGATGACAGCTCCAGAAACAGGTTCTCCAGAACTGAGCTTG 634  
 QY 734 TGAAGACTGAGAGCAGCGGTGTCTATTAATCTGTGAGAGATCAGAGCTGTGGGTACT 793  
 Db 635 TGAACCTGCGGACAGCGCGGTATTAATCTGTGAGAGATCAGAGCTGTGGGTACT 691  
 QY 794 ATGACCACTACTACGCTTTGAGAGTGTGGGCAAGAGACAGCGTCAACCTCTCTCAG 853  
 Db 692 ACAGCTATGTTACGGGATAGACTACTGTGGGCGCAGGAAACCTGTGACCTCTCTCAG 751  
 QY 854 G-----ATCCGAACAATACTGATCAGGAGAAAGATCTGAACCATCAACATCAC 903  
 Db 752 GGAAGTCACTCCGCCCAACCTTTTCCCGGGCGCAGATCATCATCACTCAC 807

RESULT 10  
 AR139121/c 450 bp DNA linear PAT 16-JUN-2001  
 LOCUS Sequence 6 from patent US 6207153.  
 DEFINITION AR139121  
 ACCESSION AR139121 GI:14481617  
 VERSION AR139121.1  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 450)  
 AUTHORS Dan,M.D., Maiti,P.K. and Kaplan,H.A.  
 TITLE Antigen binding fragments that specifically detect cancer cells,  
 nucleotides encoding the fragments, and use thereof for the  
 prophylaxis and detection of cancers  
 JOURNAL Patent: US 6207153-A 6 27-MAR-2001;  
 FEATURES Location/Qualifiers  
 source 1..450

BASE COUNT 105 a 115 c 134 g 96 t  
 ORIGIN  
 Query Match 39.3%; Score 361; DB 6; Length 450;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-90;  
 Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 GATATTGTGTAGCGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGAAAGGCCACC 129  
 Db 73 GATATTGTGTAGCGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGAAAGGCCACC 132  
 QY 130 CTCTCTGAGGGCCAGTCAAGTGTAGTGAAGTACTTGAAGTGTGATCAGAGAA 189  
 Db 133 CTCTCTGAGGGCCAGTCAAGTGTAGTGAAGTACTTGAAGTGTGATCAGAGAA 192  
 QY 190 CTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGAGCCACTGGCATGCCA 249

RESULT 11  
 AR139120 450 bp DNA linear PAT 16-JUN-2001  
 LOCUS Sequence 4 from patent US 6207153.  
 DEFINITION AR139120  
 ACCESSION AR139120  
 VERSION AR139120.1 GI:14481616  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 450)  
 AUTHORS Dan,M.D., Maiti,P.K. and Kaplan,H.A.  
 TITLE Antigen binding fragments that specifically detect cancer cells,  
 nucleotides encoding the fragments, and use thereof for the  
 prophylaxis and detection of cancers  
 JOURNAL Patent: US 6207153-A 4 27-MAR-2001;  
 FEATURES Location/Qualifiers  
 source 1..450  
 BASE COUNT 96 a 135 c 115 g 104 t  
 ORIGIN  
 Query Match 39.2%; Score 359.4; DB 6; Length 450;  
 Best Local Similarity 99.7%; Pred. No. 9.5e-90;  
 Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 70 GATATTGTGTAGCGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGAAAGGCCACC 129  
 Db 73 GATATTGTGTAGCGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGAAAGGCCACC 132  
 QY 130 CTCTCTGAGGGCCAGTCAAGTGTAGTGAAGTACTTGAAGTGTGATCAGAGAA 189  
 Db 133 CTCTCTGAGGGCCAGTCAAGTGTAGTGAAGTACTTGAAGTGTGATCAGAGAA 192  
 QY 190 CTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGAGCCACTGGCATGCCA 249



Db 193 CTTGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGCGCATCTGGATGCCA 252

Qy 250 GACAGGTTCACTGCGAGTGGGTCCGGGACAGACTTCACTTCACCATCATGATGAG 309

Db 253 GACAGGTTCACTGCGAGTGGGTCCGGGACAGACTTCACTTCACCATCATGATGAG 312

Qy 310 CTTGAAGATTTTGCAGTGTATTACTGTGACAGATGATGTTAGTCACTCAGACCTCAG 369

Db 313 CTTGAAGATTTTGCAGTGTATTACTGTGACAGATGATGTTAGTCACTCAGACCTCAG 372

Qy 370 ATCAGTTCCGGGAGGAGGACAGGTGAGATCAACAGACTGTCGTCACCATCTC 429

Db 373 ATCAGTTCCGGGAGGAGGACAGGTGAGATCAACAGACTGTCGTCACCATCTC 432

Qy 430 T 430

Db 433 T 433

RESULT 12  
MMU5051 790 bp mRNA linear ROD 06-MAY-1998  
LOCUS Mus musculus VSV-IND neutralising scFv antibody fragment generated from the germline precursor of antibody V124.  
DEFINITION  
ACCESSION AU05051.1 GI:3123634  
VERSION scFv fragment; V124 antibody.  
KEYWORDS Mus musculus (house mouse)  
SOURCE  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS 1 Kalinke, U. and Lamarre, A.  
TITLE In vitro affinity maturation of VSV-specific single-chain Fv antibody fragments  
JOURNAL 2 (bases 1 to 790)  
REFERENCE  
AUTHORS Kalinke, U.  
TITLE Direct Submission  
JOURNAL Submitted (30-MAR-1998) Kalinke U., Institute of Experimental Immunology, Department of Pathology, Schmelzbergstr. 12, 8091 Zuerich, SWITZERLAND  
COMMENT  
FEATURES  
Related sequence: X97498.  
Location/Qualifiers  
1..790  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="BALB/c"  
/db\_xref="taxon:10090"  
/cell\_line="germline precursor of V124"  
/cell\_type="hybridoma"  
1..790  
misc\_feature  
/note="VSV-IND neutralising scFv fragment"  
20..31  
misc\_feature  
/note="DYKD FLAG-tag"  
29..367  
V\_region  
/note="light chain"  
368..427  
misc\_feature  
/note="(GlyGlyGlyGlySer)x4 flexible linker"  
428..778  
V\_region  
/note="heavy chain"  
BASE COUNT 183 a 191 c 234 g 182 t  
ORIGIN

Query Match 39.0%; Score 358.4; DB 10; Length 790;  
Best Local Similarity 71.6%; Pred. No. 1.8e-89;  
Matches 530; Conservative 0; Mismatches 171; Indels 39; Gaps 3;

Qy 70 GATATTGTTGAGCAGCTCCAGGACCTGCTTTGTCTCAGGGGAAAGCCACC 129

Db 29 GACATTTGATGATCAGCTTCATCTCCCTAGCTGTGAGTGGAGAGAGGTTACT 88

Qy 130 CTCTCTGACAGGCGCAGTCAAGTGTAGTAGAG-----CTACTTAGCC 174

Db 89 ATGAGCTGCAAGTCACTCAGAGCCTTTATATATGATCAATCAAAAGAACTACTTGACC 148

Qy 175 TGGTACAGAGAAAGCTGGCAGAGCTCCAGAGCTCCATCTATGAGTGCATCCACGAG 234

Db 149 TGGTACAGAGAAAGCTGGCAGAGCTTCCTAACTGCTGATTTACTGGCATCCATGAG 208

Qy 235 GCCACTGGCATGCGCAGACAGGTTCACTGAGAGTGGGTCCGGGACAGACTTCACTCAGC 294

Db 209 GAATCTGGGGTCCCTGATTCGCTTCAAGGAGAGTGAATCTGGGACAGATTTCACTCAGC 268

Qy 295 ATCAGTGACTGAGAGCTGAAAGATTTTGCAGTGTATTACTGTCAGCAGTATGAGTCA 354

Db 269 ATCAGCAGTGTGAAGGCTGAAGACCTGCGAGTTATTACTGTCAAGATATATAGCT- 326

Qy 355 CCTCAGACACTGATCATCTTTCGGGGGAGGAGCAGAGTGAATCAACGAACTGTG 414

Db 327 -----ATTACAGCTTCGAGAGGGGAGCAGAGCTGGAATTAACGTGTGTGT 373

Qy 415 GCTGCAACATCTGTCTCTGGCGGTGGCGGTTCCGAGGTGATGATGAGTGGAGTGC 474

Db 374 G-----GTGGTTCTGGGCGGCGGCGCTCCGAGGTGATCCGAGGTGAGAGT 424

Qy 475 TCCAGGTGAGCTGTGAGTGTGGGAGGCGGTGTCAGCTGAGAGTCCCTGAGA 534

Db 425 TCCGATGTGAGCTGTGAGTGTGGGAGGCTTATGTGAGCTGAGAGGTCCCGGAAA 484

Qy 535 CTCTCCGTGACAGCTCTGATTCCTCCCTCAGAACTTGTGTATGACCTGGTCCGCGAG 594

Db 485 CTCTCCGTGACAGCTCTGATTCCTCCCTCAGAACTTGTGTATGACCTGGTCCGCGAG 544

Qy 595 GCTTGAAGCAAGGGCTGAGAGTGGGTGAGCAATTATCATATGATGAGAACATTAATAC 654

Db 545 GCTTGAAGCAAGGGCTGAGAGTGGGTGAGCAATTATGATGAGAACATTAATACATAC 604

Qy 655 TAGCAGACTCCGTGAAGGCGCATTCACATCTCCAGAGACCTTCAAGAACAGCGTG 714

Db 605 TAGCAGACACAGTGAAGGCGCATTCACATCTCCAGAGACATCCCAAGAACAGCGTG 664

Qy 715 TATCTAAATATGAACACCTGAGAACCTGAGACAGCGCTCTATTCTGTGCAAGAGAT 774

Db 665 TTCTGCAAAATGACCACTTAAGGTCTGAGGACACGCGCATGTATTACTGTGCAAGATCG 724

Qy 775 CAGAGCTGTGGGTGACTA 794

Db 725 GGGGTTACTTACTTTGACTA 744

RESULT 13  
MMU124FRG 790 bp DNA linear ROD 06-MAY-1998  
LOCUS M.musculus V124 antibody VSV-Indiana neutralising scFv fragment.  
DEFINITION  
ACCESSION X97498  
VERSION X97498.1 GI:1495715  
KEYWORDS scFv fragment; V124 antibody.  
SOURCE  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS 1 Kalinke, U., Krebber, A., Krebber, C., Bucher, E., Pluckhuhn, A., Zinkernagel, R.M. and Hengartner, H.  
TITLE Monovalent single-chain Fv fragments and bivalent miniantibodies bound to vesicular stomatitis virus protect against lethal infection  
JOURNAL Eur. J. Immunol. 26 (12), 2801-2806 (1996)  
MEDLINE 97131797  
PUBMED 8977271  
REFERENCE  
AUTHORS 2 (bases 1 to 790)  
TITLE Kalinke, U.  
JOURNAL Direct Submission  
Submitted (24-APR-1996) U. Kalinke, Institute of Experimental Immunology, Department of Pathology, Schmelzbergstr. 12, 8091



[illegible]

BASE COUNT	220 a	210 c	220 g	214 t	
Query Match	37.7%	Score 346.2;	DB 12;	Length 864;	
Best Local Similarity	66.4%	Pred. No. 4,9e-86;			
Matches 593;	Conservative 0;	Mismatches 258;	Indels 42;	Gaps 5	
ORIGIN					
EQXLISEEDL"					
QY	7	ATGAAAAAACCCGATATGCCGATCGCAAGTTCAGTCTGGTGGTTGGCTACCGTTGGCGAG	66		
DB	1	ATGAAAAAGACGATATGCCATTCGATCGCAGTCGGCCGGCTTGGCTACCGTTGGCGAG	60		
QY	67	GCCGATATTGTGTGACGCGAGCTTCACAGCACCCCTGTCTTTGTCTCAGGGGAAAGAGCC	126		
DB	61	GCCGACGTCTCGGTGACCCAAATCTCTGCTCTGCTGTGATCTTCGGATGAATTTGTTC	120		
QY	127	ACCTCTTCCTCAGAGGCGCAGTCAAGTGTATGATGACAGTACTTAAGCTGTATCCAGCAG	186		
DB	121	ACCATCATGTCGACAGGCAAGCCAG---GACATGTGATCTCGTATGTTTGGTATCGACG	177		
QY	187	AAACTGGCCAGGCTCCAGAGCTCCTCATCTATGTGTGATCCACAGGGCCACTGGCATG	246		
DB	178	AAACCGAGGAATCTCTCAGCTCTGTGCTATATGTGCAACATATTTGGCAGATGGGGTTC	237		
QY	247	CCAGACAGGTTCAAGTGGAGTGGGTCCGGAGACAGCTTCACTCAACATCAGTAGACTG	306		
DB	238	CCATCAAGGTTCAAGTGGAGTGAATCTGGCACACAGTATCTCTTAAGTCAACAGACTA	297		
QY	307	GAGCCTGAAGATTTTTCAGTGTATTTACTGTGCAGCAGTATGTAGCTCACCTCAGACACCT	366		
DB	298	CAGGTTGAAGATATTGGAACCTATTACCTGTCTACAGGTTTCTAAGT-----CT	345		
QY	367	CAGATCACTTTCCGCGAGAGGACCAAGGTGAGATCAACCACTGTGCTGCACCATCT	426		
DB	346	CCGACACAGTTTGGAGCTGGACCAAGCTGAGCTCAACAGGCTCTCGCGATGATGCT	405		
QY	427	GTCCTGCGCGGTGGCGGTTCCGAGAGTGTGGATCAGGTG-----GAGGTGGCTCC	477		
DB	406	AAGAAGATGCTGCTAABAAGATGATCTTAAGAAGATGATGCTAAGAAGATGATGCTC	465		
QY	478	CAGGTGACGTTGTGTGAGTCTGGGGGAGAGCGGTGTCCAGCTCGAGAGTCTCTGAGATTC	537		
DB	466	GAAGTCCAGCTGCAGGAGTCTGGGGGAGATTAATGTGCAGCCCTGGAAGGCTCCTGCAGTTC	525		
QY	538	TTCGTGTAGGCTCTGAGTCCCTTCGAAAGCTTGTGATGTCAGCTGGGTCCGCGACGCT	597		
DB	526	TCTGCGAGCTCAGGATTCACCTTTCAGTACCTTTCAGATGCTGGGTCCGCGACGCT	585		
QY	598	CTAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAACTAATAATCTAC	657		
DB	586	CCAAGAAAGGCTGAGTGGGTGGCAACATCAATCTTGGTGGTATGAGCACTTAATCTAT	645		
QY	658	GCAGACTTCGTGAAGGGCCGATTCACCAATCTTCAGAGACACTTCCAAAGAACGGTGTAT	717		
DB	646	CCAGATTCATGAAGGGGAGATTCATCTATCTCCAGAGATTAAGCAAAAAGCACCGTATAT	705		
QY	718	CTAAATAATGAACAGCTGAGACTGAGAGACAGCGTGTCTATTACTGTGCGAGAGATCAG	777		
DB	706	CTCCAAATGACAGTCTGAGATCTTGAGACACGGCCAGTTACTATTTGTGCCAGA-----	759		
QY	778	AGCCTGTGGGTGACTATGACCACTACTACGTTTGAAGCTCTGGGGCAAGGGAGCACAG	837		
DB	760	-----CTTTCTATTCTACGTACTAGTACTGTACTTGTGACTTCTGGGGTCAAGAACTCA	813		
QY	838	GTCACCGTCTCTCAGAGATCCGAAACAAAACGATCAACGAGAAAGATTTGAA	890		
DB	814	GTCACCGTCTCTCA-----GAAACAAAGCTTATTTCCGAAAGAAAGATTTGTA	860		

Search completed: September 17, 2003, 03:49:15  
Job time : 2507 secs

**THIS PAGE BLANK (USPTO)**



XX 22-MAY-1997; 97MO-US08962.  
 PF 22-MAY-1996; 96US-0657449.  
 PR (NOVO-) NOVOPHARM BIOTECH INC.  
 PA Dan MD, Kaplan HA, Maiti PK;  
 XX MPI: 1998-018515/02.  
 DR P-PSDB; AAM40070.  
 PT Antigen binding fragment from monoclonal antibody, H11 - allows  
 PT tumour specific detection and treatment of neoplasia  
 PS Example 7; Page 90-91; 126pp; English.  
 XX This sequence encodes a human H11 monoclonal antibody single chain V  
 CC region fragment (H11-scfv) construct which is capable of forming  
 CC monomers. This construct is used to determine the ability of H11-scfv  
 CC antibody fragments to bind specifically to the C-antigen on cancer cells.  
 CC Such antigen binding fragments may be used for treating a patient with  
 CC neoplasia. It is especially useful in the detection of lymphomas and  
 CC leukemias where the tumour cells bearing the C antigen are circulating  
 CC in the patients bloodstream. The polynucleotide sequence may be used as a  
 CC primer or a probe and the encoded protein may be used in a vaccine or for  
 CC gene therapy. The human monoclonal antibody (Mab), designated H11,  
 CC specifically recognises cancerous cells. H11 is specific for  
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,  
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and  
 CC prostate adenocarcinoma.  
 SQ Sequence 918 BP; 213 A; 240 C; 264 G; 201 T; 0 other;

Query: Match 100.0%; Score 918; DB 19; Length 918;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-224;  
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATATAAAAAACCGCTATCGGATCGAGTTCGATCGGCTGGTTCCGTACCGT 60  
 DB 1 GAATTCATATAAAAAACCGCTATCGGATCGAGTTCGATCGGCTGGTTCCGTACCGT 60  
 QY 61 GCGCAGGCGGATATGTTGAGCAGAGTTCGAGGACCCCTGCTTTGTCGAGGGGAA 120  
 DB 61 GCGCAGGCGGATATGTTGAGCAGAGTTCGAGGACCCCTGCTTTGTCGAGGGGAA 120  
 QY 121 AAGAGCCACCTCTCTCCGACGAGGCGCATGAGAGTGTAGAGCACTTACCTGGTAC 180  
 DB 121 AAGAGCCACCTCTCTCCGACGAGGCGCATGAGAGTGTAGAGCACTTACCTGGTAC 180  
 QY 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGTGATCCACGAGGGCACT 240  
 DB 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGTGATCCACGAGGGCACT 240  
 QY 241 GGCATGCCAGACAGGTTCACTGAGTGGGTTCGGGACAGACTTCACTCTCACTCACT 300  
 DB 241 GGCATGCCAGACAGGTTCACTGAGTGGGTTCGGGACAGACTTCACTCTCACTCACT 300  
 QY 301 AAGACTGAGGCTGAGAGATTTTGACGTATTACTGTACAGCACTATGTAGTCACTTAC 360  
 DB 301 AAGACTGAGGCTGAGAGATTTTGACGTATTACTGTACAGCACTATGTAGTCACTTAC 360  
 QY 361 AAGACTGAGGCTGAGAGATTTTGACGTATTACTGTACAGCACTATGTAGTCACTTAC 420  
 DB 361 AAGACTGAGGCTGAGAGATTTTGACGTATTACTGTACAGCACTATGTAGTCACTTAC 420  
 QY 421 CCATCTGTCTCTGCGGCTGCGGCTTCGAGGAGTGTGATCAGGTGAGAGTGGCTCCAG 480  
 DB 421 CCATCTGTCTCTGCGGCTGCGGCTTCGAGGAGTGTGATCAGGTGAGAGTGGCTCCAG 480  
 QY 481 GTGAGCTGTGAGAGTGTGAGGAGGCGGTGTCAGGCTGGAGAGTCCCTGAGACTTCC 540  
 DB 481 GTGAGCTGTGAGAGTGTGAGGAGGCGGTGTCAGGCTGGAGAGTCCCTGAGACTTCC 540

QY 541 TGTGAGGCTGTGAGATTCCTCTTCAAGACTTTGCTATGCACTGGGCTCCGAGGCTCTA 600  
 DB 541 TGTGAGGCTGTGAGATTCCTCTTCAAGACTTTGCTATGCACTGGGCTCCGAGGCTCTA 600  
 QY 601 GGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGAGAGCACTAAATACATACGCA 660  
 DB 601 GGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGAGAGCACTAAATACATACGCA 660  
 QY 661 GACTCCGTGAAAGGGCCGATTCACCATCTCCAGAGACACTTCCAGAGACGGTGTATCTA 720  
 DB 661 GACTCCGTGAAAGGGCCGATTCACCATCTCCAGAGACACTTCCAGAGACGGTGTATCTA 720  
 QY 721 AAAATGAACAGCTTGAAGATGAGACACGGTGTCTATTACTGTCCAGAGATCAGAC 780  
 DB 721 AAAATGAACAGCTTGAAGATGAGACACGGTGTCTATTACTGTCCAGAGATCAGAC 780  
 QY 781 CTGTGGGTGATATGACCACTACTACAGGTTTGAACGCTGGGGCAAGGGACACGGTTC 840  
 DB 781 CTGTGGGTGATATGACCACTACTACAGGTTTGAACGCTGGGGCAAGGGACACGGTTC 840  
 QY 841 ACCGTCTCTCAGAGATCCGAAACAAAACCTGATCAGCGAAGAGATCTGAACCATCACCAT 900  
 DB 841 ACCGTCTCTCAGAGATCCGAAACAAAACCTGATCAGCGAAGAGATCTGAACCATCACCAT 900  
 QY 901 CACCATTTAGTGAAGCTT 918  
 DB 901 CACCATTTAGTGAAGCTT 918

## RESULT 2

AAD04537  
 ID AAD04537 standard; DNA; 918 BP.

XX AAD04537;  
 XX 04-JUL-2001 (first entry)

XX Human monoclonal antibody H11-single chain variable region (scfv) DNA #1.  
 XX  
 XX Human; monoclonal antibody; Mab; H11; single chain variable region; scfv;  
 KW neoplastic disease; melanoma; immunoglobulin Igm; gene therapy; lymphoma;  
 KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;  
 KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;  
 KW C-antigen; chronic leukaemia; glioma; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS

FT 1..918  
 FT /\*tag= a  
 FT /product= "Human H11-single chain variable region (scfv)"  
 FT /transl\_except= (pos:904..915, aa:His-Lys)  
 FT /note= "insertion of two inframe stop codon alters the  
 FT reading frame; CDS does not include start and stop  
 FT codons"  
 FT /partial  
 FT 430..474  
 FT /\*tag= b  
 FT /note= "Encodes (SGGG) 3 linker sequence"

PN US6207153-B1.

XX 27-MAR-2001.

XX 22-MAY-1997; 97US-0862124.

XX 22-MAY-1996; 96US-0657449.

XX (VIVE-) VIVENTIA BIOTECH INC.

XX Dan MD, Maiti PK, Kaplan HA;







Query Match 87.1%; Score 799.6; DB 19; Length 867;  
 Best Local Similarity 94.0%; Pred. No. 3.9e-194;  
 Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

```

OY 1 GAATTCAGAAAAAACCCTATCGCGATGCGAGTTGACCTGGCGTGGTTCACCGTT 60
DB 1 GAATTCAGAAAAAACCCTATCGCGATGCGAGTTGACCTGGCGTGGTTCACCGTT 60
OY 61 GCGGAGCCGATATATGTTGTCAGCAGTCTCCAGGACACCTGTCTTGTCTCCAGGGAA 120
DB 61 GCGGAGCCGATATATGTTGTCAGCAGTCTCCAGGACACCTGTCTTGTCTCCAGGGAA 120
OY 121 AGAGCCACCTCTCTCGAGGGCCAGTCAGAGTTAGTAGAGCTACTTACCTGTGAC 180
DB 121 AGAGCCACCTCTCTCGAGGGCCAGTCAGAGTTAGTAGAGCTACTTACCTGTGAC 180
OY 181 CAGAGAAACCTGCGCAGGCTCCAGGCTCCATCTATGTCATCCACAGGGCCACT 240
DB 181 CAGAGAAACCTGCGCAGGCTCCAGGCTCCATCTATGTCATCCACAGGGCCACT 240
OY 241 GGCATGCGAGACAGGTTGAGTGGGTCGGGAGACACTTCACTCCACATCAGT 300
DB 241 GGCATGCGAGACAGGTTGAGTGGGTCGGGAGACACTTCACTCCACATCAGT 300
OY 301 AGACTGAGCCTGAAGATTTTGCAGTGTATTACTGTCAAGAGTATGTAAGTCACTCAG 360
DB 301 AGACTGAGCCTGAAGATTTTGCAGTGTATTACTGTCAAGAGTATGTAAGTCACTCAG 360
OY 361 ACACCTCGATCACTTTGGGCGGAGGACCAAGGTGAGATCAACGAATGTGCTGCA 420
DB 361 ACACCTCGATCACTTTGGGCGGAGGACCAAGGTGAGATCAACGAATGTGCTGCA 420
OY 421 CCATCTGCTCTGGCGGTGGCGGTTCCGAGGTGTGATCAGTGAAGTGCCTCCAG 480
DB 421 TC-----CGGAGG 429
OY 481 GTGCGAGTGTGAGACTGTGGGGAGGCGGTGTGCAGCCTGGAGAGTCCCTGAGACTCC 540
DB 481 GTGCGAGTGTGAGACTGTGGGGAGGCGGTGTGCAGCCTGGAGAGTCCCTGAGACTCC 540
OY 541 TGTGCAAGCTCTGATTTCCCTTCAGAACTTGTGTAAGCACTGGGTCCGCAAGCTCTA 600
DB 541 TGTGCAAGCTCTGATTTCCCTTCAGAACTTGTGTAAGCACTGGGTCCGCAAGCTCTA 600
OY 601 GGCAGAGGGCTGAGTGGGTGCGAGTTATCATATGATGAGCACTAAATCTACGCA 660
DB 601 GGCAGAGGGCTGAGTGGGTGCGAGTTATCATATGATGAGCACTAAATCTACGCA 660
OY 661 GACTCCGTGAAGGGCCGATTCACATCTCCAGAGACACTTCCAGAAACCGGTATCTA 720
DB 661 GACTCCGTGAAGGGCCGATTCACATCTCCAGAGACACTTCCAGAAACCGGTATCTA 720
OY 721 AAAATGAACAGCTGAGAACTGAGAGACACGGCTGTCTTACTGTCCAGAGATCAAGC 780
DB 721 AAAATGAACAGCTGAGAACTGAGAGACACGGCTGTCTTACTGTCCAGAGATCAAGC 780
OY 781 CTGTTGGGTGACTAGACCACTACTAGGTTTGAAGTCTGGGGCAAGGGACCGGTC 840
DB 781 CTGTTGGGTGACTAGACCACTACTAGGTTTGAAGTCTGGGGCAAGGGACCGGTC 840
OY 841 ACCGTCTCTCAGATTCGGAACAAAACCTGATCAGCGAAGAGATCTGAACCATCAGAT 900
DB 841 ACCGTCTCTCAGATTCGGAACAAAACCTGATCAGCGAAGAGATCTGAACCATCAGAT 900
OY 901 CACCATTTAGTAAAGCTT 918
DB 901 CACCATTTAGTAAAGCTT 918
OY 918 CACCATTTAGTAAAGCTT 918
DB 918 CACCATTTAGTAAAGCTT 918
OY 919 CACCATTTAGTAAAGCTT 918
DB 919 CACCATTTAGTAAAGCTT 918
OY 920 CACCATTTAGTAAAGCTT 918
DB 920 CACCATTTAGTAAAGCTT 918
OY 921 CACCATTTAGTAAAGCTT 918
DB 921 CACCATTTAGTAAAGCTT 918
OY 922 CACCATTTAGTAAAGCTT 918
DB 922 CACCATTTAGTAAAGCTT 918
OY 923 CACCATTTAGTAAAGCTT 918
DB 923 CACCATTTAGTAAAGCTT 918
OY 924 CACCATTTAGTAAAGCTT 918
DB 924 CACCATTTAGTAAAGCTT 918
OY 925 CACCATTTAGTAAAGCTT 918
DB 925 CACCATTTAGTAAAGCTT 918
OY 926 CACCATTTAGTAAAGCTT 918
DB 926 CACCATTTAGTAAAGCTT 918
OY 927 CACCATTTAGTAAAGCTT 918
DB 927 CACCATTTAGTAAAGCTT 918
OY 928 CACCATTTAGTAAAGCTT 918
DB 928 CACCATTTAGTAAAGCTT 918
OY 929 CACCATTTAGTAAAGCTT 918
DB 929 CACCATTTAGTAAAGCTT 918
OY 930 CACCATTTAGTAAAGCTT 918
DB 930 CACCATTTAGTAAAGCTT 918
OY 931 CACCATTTAGTAAAGCTT 918
DB 931 CACCATTTAGTAAAGCTT 918
OY 932 CACCATTTAGTAAAGCTT 918
DB 932 CACCATTTAGTAAAGCTT 918
OY 933 CACCATTTAGTAAAGCTT 918
DB 933 CACCATTTAGTAAAGCTT 918
OY 934 CACCATTTAGTAAAGCTT 918
DB 934 CACCATTTAGTAAAGCTT 918
OY 935 CACCATTTAGTAAAGCTT 918
DB 935 CACCATTTAGTAAAGCTT 918
OY 936 CACCATTTAGTAAAGCTT 918
DB 936 CACCATTTAGTAAAGCTT 918
OY 937 CACCATTTAGTAAAGCTT 918
DB 937 CACCATTTAGTAAAGCTT 918
OY 938 CACCATTTAGTAAAGCTT 918
DB 938 CACCATTTAGTAAAGCTT 918
OY 939 CACCATTTAGTAAAGCTT 918
DB 939 CACCATTTAGTAAAGCTT 918
OY 940 CACCATTTAGTAAAGCTT 918
DB 940 CACCATTTAGTAAAGCTT 918
OY 941 CACCATTTAGTAAAGCTT 918
DB 941 CACCATTTAGTAAAGCTT 918
OY 942 CACCATTTAGTAAAGCTT 918
DB 942 CACCATTTAGTAAAGCTT 918
OY 943 CACCATTTAGTAAAGCTT 918
DB 943 CACCATTTAGTAAAGCTT 918
OY 944 CACCATTTAGTAAAGCTT 918
DB 944 CACCATTTAGTAAAGCTT 918
OY 945 CACCATTTAGTAAAGCTT 918
DB 945 CACCATTTAGTAAAGCTT 918
OY 946 CACCATTTAGTAAAGCTT 918
DB 946 CACCATTTAGTAAAGCTT 918
OY 947 CACCATTTAGTAAAGCTT 918
DB 947 CACCATTTAGTAAAGCTT 918
OY 948 CACCATTTAGTAAAGCTT 918
DB 948 CACCATTTAGTAAAGCTT 918
OY 949 CACCATTTAGTAAAGCTT 918
DB 949 CACCATTTAGTAAAGCTT 918
OY 950 CACCATTTAGTAAAGCTT 918
DB 950 CACCATTTAGTAAAGCTT 918
OY 951 CACCATTTAGTAAAGCTT 918
DB 951 CACCATTTAGTAAAGCTT 918
OY 952 CACCATTTAGTAAAGCTT 918
DB 952 CACCATTTAGTAAAGCTT 918
OY 953 CACCATTTAGTAAAGCTT 918
DB 953 CACCATTTAGTAAAGCTT 918
OY 954 CACCATTTAGTAAAGCTT 918
DB 954 CACCATTTAGTAAAGCTT 918
OY 955 CACCATTTAGTAAAGCTT 918
DB 955 CACCATTTAGTAAAGCTT 918
OY 956 CACCATTTAGTAAAGCTT 918
DB 956 CACCATTTAGTAAAGCTT 918
OY 957 CACCATTTAGTAAAGCTT 918
DB 957 CACCATTTAGTAAAGCTT 918
OY 958 CACCATTTAGTAAAGCTT 918
DB 958 CACCATTTAGTAAAGCTT 918
OY 959 CACCATTTAGTAAAGCTT 918
DB 959 CACCATTTAGTAAAGCTT 918
OY 960 CACCATTTAGTAAAGCTT 918
DB 960 CACCATTTAGTAAAGCTT 918
OY 961 CACCATTTAGTAAAGCTT 918
DB 961 CACCATTTAGTAAAGCTT 918
OY 962 CACCATTTAGTAAAGCTT 918
DB 962 CACCATTTAGTAAAGCTT 918
OY 963 CACCATTTAGTAAAGCTT 918
DB 963 CACCATTTAGTAAAGCTT 918
OY 964 CACCATTTAGTAAAGCTT 918
DB 964 CACCATTTAGTAAAGCTT 918
OY 965 CACCATTTAGTAAAGCTT 918
DB 965 CACCATTTAGTAAAGCTT 918
OY 966 CACCATTTAGTAAAGCTT 918
DB 966 CACCATTTAGTAAAGCTT 918
OY 967 CACCATTTAGTAAAGCTT 918
DB 967 CACCATTTAGTAAAGCTT 918
OY 968 CACCATTTAGTAAAGCTT 918
DB 968 CACCATTTAGTAAAGCTT 918
OY 969 CACCATTTAGTAAAGCTT 918
DB 969 CACCATTTAGTAAAGCTT 918
OY 970 CACCATTTAGTAAAGCTT 918
DB 970 CACCATTTAGTAAAGCTT 918
OY 971 CACCATTTAGTAAAGCTT 918
DB 971 CACCATTTAGTAAAGCTT 918
OY 972 CACCATTTAGTAAAGCTT 918
DB 972 CACCATTTAGTAAAGCTT 918
OY 973 CACCATTTAGTAAAGCTT 918
DB 973 CACCATTTAGTAAAGCTT 918
OY 974 CACCATTTAGTAAAGCTT 918
DB 974 CACCATTTAGTAAAGCTT 918
OY 975 CACCATTTAGTAAAGCTT 918
DB 975 CACCATTTAGTAAAGCTT 918
OY 976 CACCATTTAGTAAAGCTT 918
DB 976 CACCATTTAGTAAAGCTT 918
OY 977 CACCATTTAGTAAAGCTT 918
DB 977 CACCATTTAGTAAAGCTT 918
OY 978 CACCATTTAGTAAAGCTT 918
DB 978 CACCATTTAGTAAAGCTT 918
OY 979 CACCATTTAGTAAAGCTT 918
DB 979 CACCATTTAGTAAAGCTT 918
OY 980 CACCATTTAGTAAAGCTT 918
DB 980 CACCATTTAGTAAAGCTT 918
OY 981 CACCATTTAGTAAAGCTT 918
DB 981 CACCATTTAGTAAAGCTT 918
OY 982 CACCATTTAGTAAAGCTT 918
DB 982 CACCATTTAGTAAAGCTT 918
OY 983 CACCATTTAGTAAAGCTT 918
DB 983 CACCATTTAGTAAAGCTT 918
OY 984 CACCATTTAGTAAAGCTT 918
DB 984 CACCATTTAGTAAAGCTT 918
OY 985 CACCATTTAGTAAAGCTT 918
DB 985 CACCATTTAGTAAAGCTT 918
OY 986 CACCATTTAGTAAAGCTT 918
DB 986 CACCATTTAGTAAAGCTT 918
OY 987 CACCATTTAGTAAAGCTT 918
DB 987 CACCATTTAGTAAAGCTT 918
OY 988 CACCATTTAGTAAAGCTT 918
DB 988 CACCATTTAGTAAAGCTT 918
OY 989 CACCATTTAGTAAAGCTT 918
DB 989 CACCATTTAGTAAAGCTT 918
OY 990 CACCATTTAGTAAAGCTT 918
DB 990 CACCATTTAGTAAAGCTT 918
OY 991 CACCATTTAGTAAAGCTT 918
DB 991 CACCATTTAGTAAAGCTT 918
OY 992 CACCATTTAGTAAAGCTT 918
DB 992 CACCATTTAGTAAAGCTT 918
OY 993 CACCATTTAGTAAAGCTT 918
DB 993 CACCATTTAGTAAAGCTT 918
OY 994 CACCATTTAGTAAAGCTT 918
DB 994 CACCATTTAGTAAAGCTT 918
OY 995 CACCATTTAGTAAAGCTT 918
DB 995 CACCATTTAGTAAAGCTT 918
OY 996 CACCATTTAGTAAAGCTT 918
DB 996 CACCATTTAGTAAAGCTT 918
OY 997 CACCATTTAGTAAAGCTT 918
DB 997 CACCATTTAGTAAAGCTT 918
OY 998 CACCATTTAGTAAAGCTT 918
DB 998 CACCATTTAGTAAAGCTT 918
OY 999 CACCATTTAGTAAAGCTT 918
DB 999 CACCATTTAGTAAAGCTT 918
OY 1000 CACCATTTAGTAAAGCTT 918
DB 1000 CACCATTTAGTAAAGCTT 918

```

AA04539;  
 04-JUL-2001 (first entry)

Human monoclonal antibody H11-single chain variable region (scFv) DNA #2.

Human; monoclonal antibody; Mab; H11; single chain variable region; scFv; neoplastic disease; melanoma; immunoglobulin IGM; gene therapy; lymphoma; carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine; neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic; C-antigen; chronic leukaemia; glioma; dr.

Homo sapiens.

Key CDS

Location/Qualifiers

1..867

/\*tag= a

/product= "Human H11-single chain variable region (scFv)"

/trans\_except= (pos:853..864, aa:His-Lys)

/note= "insertion of two inframe stop codon alters the reading frame; CDS does not include start and stop codons"

/partial

US6207153-B1.

27-MAR-2001.

22-MAY-1997; 97US-0862124.

22-MAY-1996; 96US-0657449.

(VIVE) VIVENTIA BIOTECH INC.

Dan MD, Maici PK, Kaplan HA;

WPI; 2001-289584/30.

P-PSDB; AAE00948.

Composition comprising antigen binding fragments of an antibody that recognizes an antigen on neoplastic cells but not on normal cells for use in diagnosis, imaging and treatment of carcinomas

Example 7; Column 67-70; 56bp; English.

The present DNA sequence encodes human monoclonal antibody (Mab), H11-single chain variable region (scFv). The H11 light chain variable region is linked to the heavy chain variable region through a (SGGGG)3 linker to form dimers.

The invention relates to human monoclonal antibody (Mab) H11, H11-(scFv) single chain variable (V) region fragment and their corresponding DNA molecules. H11 antibody is an immunoglobulin of IGM subclass which is specific to C-antigen found specifically on neoplastic cells and not on normal cells. H11 is an antibody obtained from the fusion of peripheral blood lymphocytes of a 64 year old male with a low grade glioma and fused to a human myeloma cell line to produce a hybridoma designated NBGM1/H11.

A pharmaceutical composition comprising H11 and its derivatives are useful in the diagnosis, imaging and treatment of neoplastic disease, particularly, melanoma, breast carcinoma, lung carcinoma, ovarian carcinoma, colon carcinoma, gastric carcinoma, prostate carcinoma, lymphoma carcinoma, neuroblastoma, glioma, soft tissue sarcoma, small cell lung carcinoma, prostatic adenocarcinoma, B and T cell lymphomas and chronic leukemias. H11 DNA is also used in vaccines and gene therapy.

Sequence 867 BP; 209 A; 229 C; 241 G; 188 T; 0 other;

Query Match 87.1%; Score 799.6; DB 22; Length 867;  
 Best Local Similarity 94.0%; Pred. No. 3.9e-194;  
 Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

```

OY 1 GAATTCAGAAAAAACCCTATCGCGATGCGAGTTGACCTGGCGTGGTTCACCGTT 60

```

```

Db      1 GAATTCATGAAAAAACCCTATCGCATGCGAGTTGCACTGGGCTGTTCCGTCACGTT 60
QY      61 GGGCAGGCGCGATATGTTGATGAGCTCCAGGACCCCTGCTTTGCTCCAGGGGAA 120
Db      61 GGGCAGGCGCGATATGTTGATGAGCTCCAGGACCCCTGCTTTGCTCCAGGGGAA 120
QY      121 AGAGCCACCCCTCTCTGCGAGGGCCAGTCAAGAGTTAGTAGCACTACTAGCTGTATC 180
Db      121 AGAGCCACCCCTCTCTGCGAGGGCCAGTCAAGAGTTAGTAGCACTACTAGCTGTATC 180
QY      181 CAGCAGAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGGCCACT 240
Db      181 CAGCAGAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGGCCACT 240
QY      241 GGCATGCCAGACAGTTTCAGTGGGTCCGGACAGACTTCACTCCACCACT 300
Db      241 GGCATGCCAGACAGTTTCAGTGGGTCCGGACAGACTTCACTCCACCACT 300
QY      301 AGACTGAGCCTGAAAGATTTTTCAGTGTATTACTGTCAAGCATATGTTAGCTCAG 360
Db      301 AGACTGAGCCTGAAAGATTTTTCAGTGTATTACTGTCAAGCATATGTTAGCTCAG 360
QY      361 ACACTCAATCACTTTTGGCGGAGGACCAAGTGGAGATCAACGAACCTGTGCTGCA 420
Db      361 ACACTCAATCACTTTTGGCGGAGGACCAAGTGGAGATCAACGAACCTGTGCTGCA 420
QY      421 CCATCTGTCTGGCGGTGGCGGTTCCGAGGTTGATCAAGTGGAGTGGCTCCGAG 480
Db      421 TC-----CGAGCAG 429
QY      481 GTGCAGCTGTGAGTCTGGGGGAGGCGTGTCCAGCTCGGAGGATCCTCGAGACTTCC 540
Db      430 GTGCAGCTGTGAGTCTGGGGGAGGCGTGTCCAGCTCGGAGGATCCTCGAGACTTCC 489
QY      541 TGTGCAAGCTCTGTGATTTCCCTTTCAGAACTTGTCTATGATGATGATGATGATGAT 600
Db      490 TGTGCAAGCTCTGTGATTTCCCTTTCAGAACTTGTCTATGATGATGATGATGATGAT 549
QY      601 GGCAGAGGGCTGAGTGGGTGGGAGTTATATCATATGATGAGGACCTAAATATATACGA 660
Db      550 GGCAGAGGGCTGAGTGGGTGGGAGTTATATCATATGATGAGGACCTAAATATATACGA 609
QY      661 GACTCCGTGAGAGGCGGATTCACATCTCCAGAGCACTTCCAGAGCAAGGCTGATCTTA 720
Db      610 GACTCCGTGAGAGGCGGATTCACATCTCCAGAGCACTTCCAGAGCAAGGCTGATCTTA 669
QY      721 AAAATGAACAGCTGAGAACTGAGACAGCGCTCTTATTACTGTGCCAGATCAGAGC 780
Db      670 AAAATGAACAGCTGAGAACTGAGACAGCGCTCTTATTACTGTGCCAGATCAGAGC 729
QY      781 CTGTTGGGTGATATGACACTACTACGCTTGTGAGAGTCTGGGGGCAAGAGCAAGGTC 840
Db      730 CTGTTGGGTGATATGACACTACTACGCTTGTGAGAGTCTGGGGGCAAGAGCAAGGTC 789
QY      841 ACCGTCTCTCAGATCCGAGCAAAAACCTGATCAGGGAAGAAATCTGAACCATCAACAT 900
Db      790 ACCGTCTCTCAGATCCGAGCAAAAACCTGATCAGGGAAGAAATCTGAACCATCAACAT 849
QY      901 CACCATTAATGAAGCTT 918
Db      850 CACCATTAATGAAGCTT 867

```

## RESULT 6

AA04540/C  
ID AA04540 standard; DNA; 867 BP.

XX AA04540;

XX 04-JUL-2001 (first entry)

XX Human H11-single chain variable region (scFv) complementary DNA #2.  
XX

```

KW Human; monoclonal antibody; Mab; H11; single chain variable region; scFv;
KW neoplastic disease; melanoma; immunoglobulin IgM; gene therapy; lymphoma;
KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;
KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;
KW C-antigen; chronic leukemia; glioma; ds.
XX
OS Homo sapiens.
XX
PN US6207153-B1.
XX
PD 27-MAR-2001.
XX
PF 22-MAY-1997; 97US-0862124.
XX
PR 22-MAY-1996; 96US-0657449.
XX
PA (VIVE-) VIVENTIA BIOTECH INC.
XX
PI Dan MD, Maiti PK, Kaplan HA;
XX
DR WPI; 2001-289584/30.
XX
PS Example 7; Column 71-72; 56bp; English.
XX
PT Composition comprising antigen binding fragments of an antibody that
PT recognizes an antigen on neoplastic cells but not on normal cells for
PT use in diagnosis, imaging and treatment of carcinomas
XX
The present sequence is human monoclonal antibody (Mab), H11-single chain
variable region (scFv) complementary DNA.
CC The invention relates to human monoclonal antibody (Mab) H11, H11-(scFv)
CC single chain variable (V) region fragment and their corresponding DNA
CC molecules. H11 antibody is an immunoglobulin of IgM subclass which is
CC specific to C-antigen found specifically on neoplastic cells and not on
CC normal cells. H11 is an antibody obtained from the fusion of peripheral
CC blood lymphocytes of a 64 year old male with a low grade glioma and fused
CC to a human myeloma cell line to produce a hybridoma designated NBGM1/H11.
CC A pharmaceutical composition comprising H11 and its derivatives are
CC useful in the diagnosis, imaging and treatment of neoplastic disease,
CC particularly, melanoma, breast carcinoma, lung carcinoma, ovarian
CC carcinoma, colon carcinoma, gastric carcinoma, prostate carcinoma,
CC lymphoma, neuroblastoma, glioma, soft tissue sarcoma, small
CC cell lung carcinoma, prostatic adenocarcinoma, B and T cell lymphomas
CC and chronic leukemias. H11 DNA is also used in vaccines and gene
XX therapy.
SQ Sequence 867 BP; 189 A; 241 C; 229 G; 208 T; 0 other;
XX
Query Match 86.9%; Score 798; DB 22; Length 867;
Best Local Similarity 93.9%; Pred. No. 1e-193;
Matches 862; Conservative 0; Mismatches 5; Indels 51; Gaps 1,
QY 1 GAATTCATGAAAAAACCCTATGCGATGCGAGTTGCACTGGGCTGTTGCTACCGTT 60
Db 867 GAATTCATGAAAAAACCCTATGCGATGCGAGTTGCACTGGGCTGTTGCTACCGTT 808
QY 61 GGCAGAGCGCGATATGTTGATGAGCTCCAGGACCCCTGCTTTGCTCCAGGGGAA 120
Db 807 GGCAGAGCGCGATATGTTGATGAGCTCCAGGACCCCTGCTTTGCTCCAGGGGAA 748
QY 121 AGAGCCACCCCTCTCTGCGAGGGCCAGTCAAGAGTTAGTAGCACTACTAGCTGTATC 180
Db 747 AGAGCCACCCCTCTCTGCGAGGGCCAGTCAAGAGTTAGTAGCACTACTAGCTGTATC 688
QY 181 CAGCAGAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGGCCACT 240
Db 687 CAGCAGAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGGCCACT 628
QY 241 GGCATGCCAGACAGTTTCAGTGGGTCCGGACAGACTTCACTCCACCACT 300
Db 627 GGCATGCCAGACAGTTTCAGTGGGTCCGGACAGACTTCACTCCACCACT 568
QY 301 AGACTGAGCCTGAAAGATTTTTCAGTGTATTACTGTCAAGCATATGTTAGCTCAG 360

```

```

Db      567 AGACTGGAGCCCTGGAAGATTTTGACGTATTACTGTACGACATAGTAGCTCACCTCAG 508
Qy      361 ACACCTCAGATCACTTTGCGCGAGGAGCAAGGTGAGATCAAGAACTGTGCTGCA 420
Db      507 ACACCTCAGATCACTTTGCGCGAGGAGCAAGGTGAGATCAAGAACTGTGCTGCA 448
Qy      421 CCATCTGTCTCTGCGCGGTTCGAGGTGTGATCAGTGGAGCTGCCAG 480
Db      447 TC-----CGGACAG 439
Qy      481 GTGACGCTGTGAGATCTGGGGAGGCGTGTCCAGCCTGGGAGGTCCCTGAGATCTTCC 540
Db      438 GTGACGCTGTGAGATCTGGGGAGGCGTGTCCAGCCTGGGAGGTCCCTGAGATCTTCC 379
Qy      541 TGTGACGCTGTGAGATCTTCCCTTCAAGACTTGTCTATGACACTGGGTCGCGACGCTCTA 600
Db      378 TGTGACGCTGTGAGATCTTCCCTTCAAGACTTGTCTATGACACTGGGTCGCGACGCTCTA 319
Qy      601 GGCAGAGGGGCTGAGATGGGTGGCACTTATCATATGATGAGAGCACTAAATACTACGCA 660
Db      318 GGCAGAGGGGCTGAGATGGGTGGCACTTATCATATGATGAGAGCACTAAATACTACGCA 259
Qy      661 GACTCCCTGAGAGGGCCGATTCACCATCTCCAGAGACACTTCCAGAAACACGGGTATCTA 720
Db      258 GACTCCCTGAGAGGGCCGATTCACCATCTCCAGAGACACTTCCAGAAACACGGGTATCTA 199
Qy      721 AAAATGAACAGCCTGAGAACTGAGGACACGGCTGTCTATCTGTGCGAGATCAGAGC 780
Db      198 AAAATGAACAGCCTGAGAACTGAGGACACGGCTGTCTATCTGTGCGAGATCAGAGC 139
Qy      781 CTGTTGGGTGACTATGACACTACTACGCTTGTGACGTCTGTGGGCAAGGACACGGTTC 840
Db      138 CTGTTGGGTGACTATGACACTACTACGCTTGTGACGTCTGTGGGCAAGGACACGGTTC 79
Qy      841 ACCGCTCTCTCAGATCCGAAACAAACTGATCAGCGAAGAAATCTGAACTATACCAT 900
Db      78  ACCGCTCTCTCAGATCCGAAACAAACTGATCAGCGAAGAAATCTGAACTATACCAT 19
Qy      901 CACCATAGTGAAGCTT 918
Db      18 CACCATAGTGAAGCTT 1

```

RESULT 7  
AAZ50587  
ID AAZ50587 standard; DNA; 1630 BP.  
XX  
AAZ50587;  
XX  
23-MAY-2000 (first entry)  
XX  
HD70scFv-CH1-GM-CSF chain encoding DNA.  
DE  
XX HD70scFv-CH1-GM-CSF chain encoding DNA.  
XX  
HD70; single-chain variable fragment; scFv; 17-1A antigen; human;  
KM EpcAM; epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;  
KM granulocyte/macrophage colony stimulating factor; heteromultibody;  
KM CH1-domain; multifunctional compound; heavy chain constant domain;  
KM immunoglobulin; cytototoxic; immunostimulatory; antileukemia; diagnosis;  
KM antiproliferative; prevention; treatment; malignant; haematopoietic cell;  
KM lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma; dc.  
XX  
OS Homo sapiens.  
XX  
Key Location/Qualifiers  
FT CDS 39..1610  
FT /tag= a  
FT /product= "HD70scFv-CH1-GM-CSF chain"  
FT misc\_feature 96..842  
FT /tag= b  
FT /label= HD70\_scFv  
XX  
FN MO200006605-A2.

```

XX      10-FEB-2000.
PD      28-JUL-1999; 99WO-EP05416.
XX      28-JUL-1998; 98EP-0114082.
XX      28-JUL-1998; 98EP-0114082.
XX      (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
PA      Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;
PI      WPI; 2000-195265/17.
DR      P-PSDB; AA44994.
XX      New multifunctional compounds useful for preventing and/or treating
PT      malignant cell growth and for detection and diagnosis
XX      Claim 8; Fig 55a; 16pp; English.
PS      The patent discloses heteromultibodies which are multifunctional compounds
XX      producible in a mammalian host cell as a secretable and fully functional
CC      heterodimer of two polypeptide chains, where one of the polypeptide
CC      chains comprises a CH1-domain (constant domain of an immunoglobulin
CC      heavy chain) and the other chain comprises CL-domain (constant domain of
CC      an immunoglobulin light chain). The polypeptide chains further comprise,
CC      fused to the constant domains at least two (polypeptides having
CC      different receptor or ligand functions, where further at least two of the
CC      different (polypeptides) lack an intrinsic affinity for one another and
CC      are linked via the constant domains. The heteromultibodies have
CC      cytototoxic, immunostimulatory, antileukemia and antiproliferative
CC      activities. These compounds can be used for diagnosing, preventing and
CC      treating malignant cell growth related to malignancies of haematopoietic
CC      cells e.g. lymphomas and leukemias, or to solid tumours e.g. carcinomas,
CC      melanomas and sarcomas.
CC      The present sequence is a DNA encoding left chain of a heteromultibody
CC      comprising HD70 single-chain Fv (scFv) fragment N-terminally linked to
CC      human CH1 domain which bears at its C-terminus the human inflammatory
CC      cytokine granulocyte/macrophage colony stimulating factor (GM-CSF), plus
CC      a hexahistidine sequence for ease of purification. HD70 scFv
CC      specifically recognises the human epithelial cell adhesion molecule
CC      (EpcAM) also called 17-1A antigen.
XX      Sequence 1630 BP; 376 A; 484 C; 437 G; 333 T; 0 other;
SQ

```

Query Match 48.5%; Score 445; DB 21; Length 1630;  
Best Local Similarity 76.3%; Pred. No. 1.3e-103;  
Matches 620; Conservative 0; Mismatches 145; Indels 48; Gaps 4;

```

Qy      52 GCTACCGTTGCGAGCGCGATATTTGTTGACGACGCTCCAGGACACCTGCTTGTCT 111
Db      78 GCTACAGGTGTACACTCCGACCTCCAGATGACCCAGTCTCATCTCTCTGTCATCT 137
Qy      112 CCAGGGGAAAGACCCACCTCTCTCTGACAGGCGCATGTCAGAGTGTATGACACTATTA 171
Db      138 GTAGAGAGCAGAGTACCATCATCTTGGCGGCAATGACAG---CATTAGACAGCTATTTA 194
Qy      172 GCCGTGTACAGAGAAACCTGGCGACAGCTCCGAGCTCCATCTATNGGCATCCACC 231
Db      195 AATTGTATTCAGCAAGAAACAGGACAGCTCTTAAGCTGCTCATTTTACTGTGGCATTAAC 254
Qy      232 AGGGCCACTGGACATGACAGACAGGTGAGTGGAGTGGGTCCGGAGACAGCTTCACTTC 291
Db      255 CGGGAATCCGGGGTCCCTGACCCGATTCAGCGCGAGTGAATTTGGAGCAAAATTACACTTC 314
Qy      292 ACATCAGTATGACTGAGAGCTGAAAGATTTTGACGTATTACTGTCAAGAGTATGTATGC 351
Db      315 ACATCAGAGAGCTGAGAGCTGAAAGATTTTGCTACTTATCTTTGTCAACACTGTGACAGT 374
Qy      352 TCACCTCAGACACTCAGATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGCAACT 411
Db      375 TTGCT-----GATTACTTGTGGCCAAAGGAGACGACTGTGACATTTCAA----- 416
Qy      412 GTGCTGACCATCTGTCTGTGCGGTGGCGGTTCCGAGGTGTGATCAGGTGAGAGT 471

```



Db 576 CAGGCTCCAGGAGGGGCTGGAGTGGGTCAGTATATCATGATGAGAAATATATA 635  
 Oy 652 TACTACGACAGACTCCGTGTAAGGGCCGATTACCATCTCCAGAGACATTCCAAGAACG 711  
 Db 636 TACTATGACAGACTCCGTGTAAGGGCCGATTACCATCTCCAGAGACAAATTCAGAACG 695  
 Oy 712 CTGTTCTTAAAAATGAACGCTTGAGAACTGAGACACGGCTGTCTATTACTGTGCGAGA 771  
 Db 696 CTGATCTGCAAAATGAACGCTTGAGAGACACGGCTGTGTATTACTGTGCGAAA 755  
 Oy 772 GATCAGAGCTGTGGTGACT-----ATGACCACTACTAGCGTTTGGACGTGGGGC 825  
 Db 756 GATATGGGGTGGGGCAGATGGCTGAGAACCTTACTACTACTACGATGAGACCTCTGGGC 815  
 Oy 826 AAGGAGCACCGGTCAACCGCTCTCTCAGGATCC 858  
 Db 816 CAAGGAGCACCGGTCAACCGCTCTCTCCGGAACC 848  
 RESULT 9  
 ID AAD04530/C  
 AC AAD04530 standard; DNA; 450 BP.  
 XX AAD04530;  
 DT 04-JUL-2001 (first entry)  
 XX  
 DE Human H11 antibody light chain variable region complementary DNA.  
 KM Human; monoclonal antibody; Mab; H11; light chain variable region; scFv;  
 KM single chain variable region; immunoglobulin IgM; gene therapy; lymphoma;  
 KM neoplastic disease; melanoma; carcinoma; breast; lung; gastric; prostate;  
 KM ovary; colon; lung; chronic leukaemia; neuroblastoma; vaccine; C-antigen;  
 KM soft tissue sarcoma; cytosolic; prostatic adenocarcinoma; glioma; de.  
 XX Homo sapiens.  
 OS  
 XX US6207153-B1.  
 FN  
 XX 27-MAR-2001.  
 PD  
 XX 22-MAY-1997; 97US-0862124.  
 PE  
 XX 22-MAY-1996; 96US-0657449.  
 PR  
 XX (VIVE-) VIVENTIA BIOTECH INC.  
 PA  
 XX Dan MD, Maiti PK, Kaplan HA;  
 PI  
 XX WPI; 2001-289584/30.  
 DR  
 PT Composition comprising antigen binding fragments of an antibody that  
 PT recognizes an antigen on neoplastic cells but not on normal cells for  
 PT use in diagnosis, imaging and treatment of carcinomas  
 PT  
 XX Disclosure; Column 59-60; 56pp; English.  
 PS  
 XX The present sequence is human monoclonal antibody (Mab), H11 light chain  
 CC variable region complementary DNA.  
 CC The invention relates to human monoclonal antibody (Mab) H11, H11-(scFv)  
 CC single chain variable (V) region fragment and their corresponding DNA  
 CC molecules. H11 antibody is an immunoglobulin of IgM subclass which is  
 CC specific to C-antigen found specifically on neoplastic cells and not on  
 CC normal cells. H11 is an antibody obtained from the fusion of peripheral  
 CC blood lymphocytes of a 64 year old male with a low grade glioma and fused  
 CC to a human myeloma cell line to produce a hybridoma designated NBGM1/H11.  
 CC A pharmaceutical composition comprising H11 and its derivatives are  
 CC useful in the diagnosis, imaging and treatment of neoplastic disease,  
 CC particularly, melanoma, breast carcinoma, lung carcinoma, ovarian  
 CC carcinoma, colon carcinoma, gastric carcinoma, prostate carcinoma,  
 CC lymphoma carcinoma, neuroblastoma, glioma, soft tissue sarcoma, small  
 CC cell lung carcinoma, prostatic adenocarcinoma, B and T cell lymphomas  
 CC and chronic leukaemias. H11 DNA is also used in vaccines and gene

CC therapy.  
 XX  
 SQ Sequence 450 BP; 105 A; 115 C; 134 G; 96 T; 0 other;  
 Query Match 39.3%; Score 361; DB 22; Length 450;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-82;  
 Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 70 GATATTGTTGTTGACCGACAGTCTCCAGCACCCCTGTCTTGTCTCCAGGGGAAAGCCACC 129  
 Db 378 GATATTGTTGTTGACCGACAGTCTCCAGCACCCCTGTCTTGTCTCCAGGGGAAAGCCACC 319  
 Oy 130 CTCTCTCGAGGGCCAGTCAAGTGTATGATGACAGCTTACTTGTGTACCAAGAGAA 189  
 Db 318 CTCTCTCGAGGGCCAGTCAAGTGTATGATGACAGCTTACTTGTGTACCAAGAGAA 259  
 Oy 190 CCGGCGAGGGCTCCAGGCTCCTCATATGTTGTGATCCACAGGGCCACTGGSCATGCCA 249  
 Db 258 CCGGCGAGGGCTCCAGGCTCCTCATATGTTGTGATCCACAGGGCCACTGGSCATGCCA 199  
 Oy 250 GACAGTTCAAGTGCAGTGGGTCCGGGACAGACTTCACTTCACCATCAGTAGACTGGAG 309  
 Db 198 GACAGTTCAAGTGCAGTGGGTCCGGGACAGACTTCACTTCACCATCAGTAGACTGGAG 139  
 Oy 310 CCTGAAGATTTTGCAGTGTATTACTGTGACAGATATGTAAGTCACTTCAGACCTTCAG 369  
 Db 138 CCTGAAGATTTTGCAGTGTATTACTGTGACAGATATGTAAGTCACTTCAGACCTTCAG 79  
 Oy 370 ATCACTTTCCGCGGAGGAGCCAAAGTGGAGATCAACGAACTGTGGCTGCACCATCTGTC 429  
 Db 78 ATCACTTTCCGCGGAGGAGCCAAAGTGGAGATCAACGAACTGTGGCTGCACCATCTGTC 19  
 Oy 430 T 430  
 Db 18 T 18  
 RESULT 10  
 ID AAV10111  
 AC AAV10111 standard; DNA; 450 BP.  
 XX AAV10111;  
 DT 29-MAY-1998 (first entry)  
 XX  
 DE Human monoclonal antibody H11 variable region H chain DNA.  
 KM H11; monoclonal antibody; Mab; C-antigen; variable region heavy chain;  
 KM V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe;  
 KM primer; vaccine; gene therapy; glioblastoma; neuroblastoma;  
 KM malignant melanoma; adenocarcinoma; small cell lung carcinoma; ss.  
 XX Homo sapiens.  
 OS  
 XX WO9744461-A2.  
 FN  
 XX 27-NOV-1997.  
 PD  
 XX 22-MAY-1997; 97WO-US08962.  
 PE  
 XX 22-MAY-1996; 96US-0657449.  
 PR  
 XX (NOVO-) NOVOPHARM BIOTECH INC.  
 PA  
 XX Dan MD, Kaplan HA, Maiti PK;  
 PI  
 XX WPI; 1998-018515/02.  
 DR  
 PT P-PSDB; AAW40069.  
 PT Antigen binding fragment from monoclonal antibody, H11 - allows  
 PT tumour specific detection and treatment of neoplasia  
 PT  
 XX Claim 29; Page 87; 126pp; English.  
 PS

XX This sequence encodes the human H11 monoclonal antibody variable (V)  
 CC region heavy (H) chain which specifically recognises the C-antigen. Such  
 CC an antigen binding fragment may be used for treating a patient with  
 CC neoplasia. It is especially useful in the detection of lymphomas and  
 CC leukaemias where the tumour cells bearing the C antigen are circulating  
 CC in the patients bloodstream. The polynucleotide sequence may be used as a  
 CC primer or a probe and the encoded protein may be used in a vaccine or  
 CC for gene therapy. The human monoclonal antibody (Mab), designated H11,  
 CC specifically recognises cancerous cells. H11 is specific for  
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,  
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and  
 CC prostate adenocarcinoma. The antigen binding fragment may also be used  
 CC to detect C-antigen in a sample.

XX Sequence 450 BP; 96 A; 135 C; 115 G; 104 T; 0 other;

Query Match 39.2%; Score 359.4; DB 19; Length 450;  
 Best Local Similarity 99.7%; Pred. No. 6.2e-82;  
 Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 70 GATATTGTGTTGACGAGTCTCCAGGACCCCTGTTTCTCCAGGGGAAAGCCACC 129  
 DB 73 GATATTGTGTTGACGAGTCTCCAGGACCCCTGTTTCTCCAGGGGAAAGCCACC 132  
 QY 130 CTCTCTCGACGGGCCAGTCAAGTGTAGTACAGCTTACCTGTGTCCAGCAGAAA 189  
 DB 133 CTCTCTCGACGGGCCAGTCAAGTGTAGTACAGCTTACCTGTGTCCAGCAGAAA 192  
 QY 190 CTTGGCAGAGCTCCAGAGCTCTCATCTATGTGTGTCATCCAGAGGCACTGGCATGCCA 249  
 DB 193 CTTGGCAGAGCTCCAGAGCTCTCATCTATGTGTGTCATCCAGAGGCACTGGCATGCCA 252  
 QY 250 GACAGGTTGAGTGGAGTGGGTCGGGACAGACTTCACTTCACCATCAGTAACTGGAG 309  
 DB 253 GACAGGTTGAGTGGAGTGGGTCGGGACAGACTTCACTTCACCATCAGTAACTGGAG 312  
 QY 310 CTTGAAGATTTTTCAGTGTATTTACTGTACAGAGTATGTAGTCACTCCAGACCTCCAG 359  
 DB 313 CTTGAAGATTTTTCAGTGTATTTACTGTACAGAGTATGTAGTCACTCCAGACCTCCAG 372  
 QY 370 ATCACTTTCGGCGAGGAGCAAGAGTGAAGATCAAGCACTGTGCTGCACCATCTGTC 429  
 DB 373 ATCACTTTCGGCGAGGAGCAAGAGTGAAGATCAAGCACTGTGCTGCACCATCTGTC 432  
 QY 430 T 430  
 DB 433 T 433

## RESULT 11

AAD04529 ID AAD04529 standard; DNA; 450 BP.

XX AAD04529;

XX 04-JUL-2001 (first entry)

XX Human monoclonal antibody (Mab), H11 light chain variable region DNA.

XX Human; monoclonal antibody; Mab; H11, light chain variable region; scfv;  
 KW single chain variable region; immunoglobulin IGM; gene therapy; lymphoma;  
 KW neoplastic disease; melanoma; carcinoma; breast; lung; gastric; prostate;  
 KW ovary; colon; chronic leukemia; neuroblastoma; vaccine; C-antigen;  
 KW soft tissue sarcoma; cytostatic; prostatic adenocarcinoma; glioma; ds.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH 1..450  
 FT /tag= a  
 FT /product= "Human H11 light chain variable region"  
 FT /transl\_except= (pos:259..261, aa:Phe)

FT /note= "CDS does not include start and stop codons"  
 FT /partial

XX US6207153-B1.

XX 27-MAR-2001.

XX 22-MAY-1997; 97US-0862124.

XX 22-MAY-1996; 96US-0657449.

XX (VIVE-) VIVENTIA BIOTECH INC.

XX Dan MD, Maiti PK, Kaplan HA;

XX WPI, 2001-289584/30.

XX P-PSDB; AAE00946.

PT Composition comprising antigen binding fragments of an antibody that  
 PT recognises an antigen on neoplastic cells but not on normal cells for  
 PT use in diagnosis, imaging and treatment of carcinomas -

XX Disclosure; Column 57-58; 56pp; English.

XX The present DNA sequence encodes human monoclonal antibody (Mab), H11  
 CC light chain variable region.

CC The invention relates to human monoclonal antibody (Mab) H11, H11-(scfv)  
 CC single chain variable (V) region fragment and their corresponding DNA  
 CC molecules. H11 antibody is an immunoglobulin of IGM subclass which is  
 CC specific to C-antigen found specifically on neoplastic cells and not on  
 CC normal cells. H11 is an antibody obtained from the fusion of peripheral  
 CC blood lymphocytes of a 64 year old male with a low grade glioma and fused  
 CC to a human myeloma cell line to produce a hybridoma designated NBGM/H11.  
 CC A pharmaceutical composition comprising H11 and its derivatives are  
 CC useful in the diagnosis, imaging and treatment of neoplastic disease,  
 CC particularly, melanoma, breast carcinoma, lung carcinoma, ovarian  
 CC carcinoma, colon carcinoma, gastric carcinoma, prostate carcinoma,  
 CC lymphoma carcinoma, neuroblastoma, glioma, soft tissue sarcoma, small  
 CC cell lung carcinoma, prostatic adenocarcinoma, B and T cell lymphomas  
 CC and chronic leukemias. H11 DNA is also used in vaccines and gene  
 CC therapy.

XX Sequence 450 BP; 96 A; 135 C; 115 G; 104 T; 0 other;

Query Match 39.2%; Score 359.4; DB 22; Length 450;  
 Best Local Similarity 99.7%; Pred. No. 6.2e-82;  
 Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 70 GATATTGTGTTGACGAGTCTCCAGGACCCCTGTTTCTCCAGGGGAAAGCCACC 129  
 DB 73 GATATTGTGTTGACGAGTCTCCAGGACCCCTGTTTCTCCAGGGGAAAGCCACC 132  
 QY 130 CTCTCTCGACGGGCCAGTCAAGTGTAGTACAGCTTACCTGTGTCCAGCAGAAA 189  
 DB 133 CTCTCTCGACGGGCCAGTCAAGTGTAGTACAGCTTACCTGTGTCCAGCAGAAA 192  
 QY 190 CTTGGCAGAGCTCCAGAGCTCTCATCTATGTGTGTCATCCAGAGGCACTGGCATGCCA 249  
 DB 193 CTTGGCAGAGCTCCAGAGCTCTCATCTATGTGTGTCATCCAGAGGCACTGGCATGCCA 252  
 QY 250 GACAGGTTGAGTGGAGTGGGTCGGGACAGACTTCACTTCACCATCAGTAACTGGAG 309  
 DB 253 GACAGGTTGAGTGGAGTGGGTCGGGACAGACTTCACTTCACCATCAGTAACTGGAG 312  
 QY 310 CTTGAAGATTTTTCAGTGTATTTACTGTACAGAGTATGTAGTCACTCCAGACCTCCAG 359  
 DB 313 CTTGAAGATTTTTCAGTGTATTTACTGTACAGAGTATGTAGTCACTCCAGACCTCCAG 372  
 QY 370 ATCACTTTCGGCGAGGAGCAAGAGTGAAGATCAAGCACTGTGCTGCACCATCTGTC 429  
 DB 373 ATCACTTTCGGCGAGGAGCAAGAGTGAAGATCAAGCACTGTGCTGCACCATCTGTC 432  
 QY 430 T 430

Db 433 T 433

## RESULT 12

AAZ57599 standard; DNA; 1574 BP.

AAZ57599;

19-APR-2000 (first entry)

Erythrocyte and Hepatitis B dual-specific antibody DNA sequence.

Erythrocyte; Hepatitis B; dual-specific antibody; surface antigen; ds.

Unidentified.

CN1232039-A.

20-OCT-1999.

02-APR-1999; 99CN-0103517.

02-APR-1999; 99CN-0103517.

(NAVA-) NAVAL GEN HOSPITAL PLA.

Chen Y, Wang Y;

WPI; 2000-098467/09.

Genetic engineering double specific antibody and its use -

Claim 1; Page 1-2; 6pp; Chinese.

The present invention describes a dual-specific antibody composed of the surface antigens to resist against erythrocyte and hepatitis B, which can be used as the test reagent to detect the surface antigen of hepatitis B in blood. The dual-specific antibody is prepared by recombination technique in gene engineering. The recombination technique includes reforming the surface antigen to resist against erythrocyte and hepatitis B to become hybrid antibody genes by shortening the joining peptide of single-chain antibody, and assembling them in the same expression vector. The gene product can be directly extracted from the supernatant of bacterial culture liquid. Its advantages are low cost, quick detection and simple operation.

Sequence 1574 BP; 395 A; 390 C; 419 G; 370 T; 0 other;

Query Match 37.7%; Score 345.8; DB 21; Length 1574;

Best Local Similarity 68.7%; Pred. No. 2.5e-78;

Matches 583; Conservative 0; Mismatches 197; Indels 69; Gaps 5;

7 ATGAAAAAACCGCTATCGCATCGAGTTGCACTGCGTGTTCGCTACCGTTCGCA- 65  
 792 ATGAAAAAGACGCTATCGCATCGAGTTGCACTGCGTGTTCGCTACCGTTCGCA- 851  
 66 --GGCCGATATTGTGTGACGAGTCTCAGGACCCCTGTCTTGTCTCCAGGGAGAA 123  
 852 GCGGCCGAGCTCCAGATGACCAAGTCTCCAGCTCCATTCGATCTGTGGAGAAACT 911  
 124 GCCACCTCTCTCGAGGGCCAGTCAGAGTGTAGAGAGCTACTTACGCTGTACAG 183  
 912 GTACACATCATGTCGAGCAAGTAGA---ATATTACAGTTATTACATGATGATCAG 968  
 184 CAGAACTGCGCAGGCTCCAGGCTCTCATCTATGTGTCATCCACGAGGCCACTGAC 243  
 969 CAGAAACAGGGAAATCTCTCAGCTCTGTCTATATGCAAAAACCTTACAGAAAGT 1028  
 244 ATGCCAGACAGTTGAGTGGCGTGGTCCGGACAGACTTCACTCTACCATCTAGTACA 303  
 1029 GTGCCATCAAGGTTCAGTGGCGAGTGTATCAGGACACAGTTTCTGTGAAGATCAACAGC 1088

QY 304 CTGAGCCTGAAGATTTTGCAGTGTATTACTGTACAGCACTATAGTAGTCACTCAGACA 363  
 DB 1089 CTGAGCCTGAAGATTTTGCAGTGTATTACTGTACCAATCATATATGTACTGCTC----- 1143  
 QY 364 CCTCAGATCACTTTGGCGGAGGACCAAGGTGAGATCAAAAGAACTGTGCTGACCA 423  
 DB 1144 -----TCACGTTCCGTCTGTGGACCAAGCTGAGCTGAACGGTCT----- 1184  
 QY 424 TCTGTCTCGGCGGTGCGGTTCCGAGGTGATGATCAGTGTGAGTGGCTCCAGGTG 483  
 DB 1185 -----AGAGGTGTGATCCAGGTGAG 1208  
 QY 484 CAGTGTGAGTCTGGGGAGGCGGTGTCAGCCTGAGAGTCCCTGAGACTTCTCTGT 543  
 DB 1209 CTGCTGAGAGACTGTGGGGAGGCTTGTGTACAGCTGGGGGCTCTTGAGACTTCTCTGT 1268  
 QY 544 GCAGCCTGTGATTCCTTCAGAAAGCTTGTGTATGCACTGAGTCCGACAGCTTAGGC 603  
 DB 1269 GCATCTCTGATTCACCTTTAGTACTATGCGGTGAGTGGGTCCGACAGGCTCTGGG 1328  
 QY 604 AAGGGCTGAGTGGTGGCACTTATATGATGATGAGACCTAAATATTCAGGAGAC 663  
 DB 1329 AAGGGCTGAGTGGTGGTCCAACTCACTGAGCAGTGTGAGAAACATATCAAGCAGAC 1388  
 QY 664 TCCGTGAAGGCGCATTCATCTCAGAGACACTTCCAGAAACAGCGTGTATCTAA 723  
 DB 1389 TCCGTGAAGGCGCATTCATCTCAGAGACACTTCCAGAAACAGCGTGTATCTGCAA 1448  
 QY 724 ATGAACAGCTGAGAACCTGAGGACAGCGTGTCTATTACTGTGCGAGAGATCAGAGCCTG 783  
 DB 1449 ATGAACAGCTGAGAACCTGAGGACAGCGGCGTATTACTGTGCGAAAGTCAAGATGTT 1508  
 QY 784 TTGGGTGACTATGACCACTACTACGTTTGAACGCTGTGGGCAAGGAGCAAGGTCAAC 843  
 DB 1509 CGGGGTGGCT---ACTGGTTTACGGTATGACGCTGTGGGCAAGGAGCCGCGGTCA 1565  
 QY 844 GTCTCTCA 852  
 DB 1566 GTCTCTCA 1574

## RESULT 13

AAT08490 standard; DNA; 783 BP.

AAT08490;

25-MAR-2003 (updated)

15-MAR-1996 (first entry)

Anti-C5 Mab M19/8 scFv (His-tagged) DNA.

Complement C5; haemolysis; kidney; glomerulonephritis;

monoclonal antibody; antiinflammatory; antibody engineering;

scFv; single chain antibody; ds.

Mus sp.

W09529697-A1.

09-NOV-1995.

01-MAY-1995; 95WO-US05688.

02-MAY-1994; 94US-0236208.

(ALEX-) ALEXION PHARM INC.

XX

PI Evans MD, Matris L, Mueller EE, Nye SH, Rollins S, Rother RP;  
 PI Springhorn JP, Squinto SP, Thomas TC, Wang Y, Wilkins JA;  
 DR WPI, 1995-392923/50.  
 DR P-PSDB; AAR7617.  
 PT Treating glomerulonephritis with antibody against complement C5  
 PT component - to inhibit complement induced cell lysis  
 PS Example 12; Page 147-149; 181pp; English.  
 XX A DNA construct (AAR08490) codes for an anti-human complement  
 CC C5 monoclonal antibody scFv (AAR7617). Unlike the native  
 CC MAb, the scFv antibody was unable to block the generation of  
 CC C5a and C5b-9 from C5. This was in contrast to a humanised  
 CC scFv (see AAR7616) generated from MAb 5G1.1.  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 783 BP; 189 A; 195 C; 217 G; 182 T; 0 other;  
 Query Match 37.4%; Score 345.2; DB 16; Length 783;  
 Best Local Similarity 69.3%; Pred. No. 38-78;  
 Matches 552; Conservative 0; Mismatches 193; Indels 51; Gaps 4;  
 QY 66 GGCCGATATGTTGTTGACGAGTCTCCAGGACCCCTGTTCTTCAGGAGAAAGAGC 125  
 DB 3 GGCCATATTGTGTGACCCCAATCTCAGCTTCTTGCTGTGTCTAGGAGAGGCG 62  
 QY 126 GACCTCTCTGCGAGGGCCAGTCAGAGTGTAGT-----CAGTACTTACCTTG 176  
 DB 63 CACCATATCTGCGAGAGCCAGTGAAGTGTGATGATGATGAGCAATGTTTATGCACTG 122  
 QY 177 GTACCGAGCAAAACCTGCGAGGCTCCAGGCTCCATCTATGAGGCAATCCAGGCG 236  
 DB 123 GTACCGAGCAAAACCTGCGAGGCTCCAGGCTCCATCTATGAGGCAATCCAGGCG 182  
 QY 237 CACTGCGATCCAGACAGTTCAGTGGTCCGAGAGAGACTTCACTCTCAACAT 296  
 DB 183 ATCTGGGGTCCCTGCGAGGTTCACTGAGTGGTCTAGAGACAGACTTCACTCAACAT 242  
 QY 297 CAGTGAAGTGGAGCTGAGATTTTGCATGTATTTACTGTCAGAGTATGATGCTCACC 356  
 DB 243 TGATCTGTGAGAGCTGATGATGTCGCAACCTATGTCAGCA-----AAA 290  
 QY 357 TCAGACACCTCATATCTTCCGCGAGAGCAAGAGTGAATCAAGAACTGTGGC 416  
 DB 291 TAATGAGTTCGAAACGTTCCGAGGGGAGCCAACTGAAATTAAGGA----- 343  
 QY 417 TGCACCATCTGCTCTGCGGCTGCGAGTTCGAGGTGTGATCAGGTGAGGTGCTC 476  
 DB 344 -----CCGAGGTGCGGCTGCGGCTGCGGAGTCCGCTGCGGAGGCTC 389  
 QY 477 CAGGTGACCTGTGAGTCTTGGGGAGGCGTGTCCAGCTCGGAGGTTCTTGAGACT 536  
 DB 390 GAGAGTCAACCTGTGAGTCTGCGGAGGAGCTTATGAAACCTTGGAGGTTCCCTGAAC 449  
 QY 537 CTCTGTGAGGCTCTGAGATTCCTCCCAAGCTTTCATGATGAGTGGTCCGCGAGC 596  
 DB 450 CTCTGTGAGGCTCTGAGATTCCTCCCAAGCTTTCATGATGAGTGGTCCGCGAGT 509  
 QY 597 TCTAGGCAAGGGGCTGAGTGGTGGAGTATATCATATGATGAGAGCACTAAATCTA 656  
 DB 510 TTTCAGAGAAAGGCTGAGTGGTGGAGTATTAATGATGATGAGAGCACTA 569  
 QY 657 CGCAGACTCGTGAAGGGCGGATTCACATCTCCAGAGACACTTCAAGAAACGCTGTA 716  
 DB 570 TCCAGACACTGTGAAGGGCGGATTCACATCTCCAGAGAAATCCAAAGAGCCTCGA 629  
 QY 717 TCTAAATAATGAAGCTGAGAACTGAGACACGCGCTGTCTATATCTGCGAGATCA 776  
 DB 630 TCTGCAATAATGAAGCTGAGAACTGAGACACGCGCTGTCTATATCTGCGAGATCA 686  
 QY 777 GAGCTGTGAGTGAATGATGACCACTAGTGTGAGTGTGAGAGTGTGAGAGGAGCAAC 836

DB 687 -----GACTATTAATGAGGATGATCCGCTCTCATGTCTGCGGAGAGGACAC 740  
 QY 837 GGTACACCTCTCTCTCA 852  
 DB 741 GGTACACCTCTCTCTCA 756  
 RESULT 14  
 ID AAT96346 standard; cDNA, 1848 BP.  
 AC AAT96346;  
 DT 08-APR-1998 (first entry)  
 XX Chimeric gene containing anti-asparaginase MAb light and heavy chain.  
 XX Immunoglobulin; Ig; heavy chain; variable region; murine; human;  
 KM asparaginase II; monoclonal antibody; MAb; light chain;  
 KM recombinant chimeric polypeptide; ss.  
 OS Synthetic.  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - Mus sp.  
 PN US686579-A.  
 PD 11-NOV-1997.  
 PF 23-MAY-1995; 95US-0447422.  
 PR 22-JUN-1993; 93US-0081410.  
 PR 21-JUN-1988; 88US-0205748.  
 PR 31-AUG-1992; 92US-0938505.  
 PR 23-MAY-1995; 95US-0447422.  
 PA (HYBR-) HYBRISSENS LTD.  
 PI Ramjessingh M, Rothelein A, Shani EY;  
 DR WPI; 1997-558200/51.  
 PT Self-protecting chimeric polypeptide comprising biologically active  
 PT sequence and single-chain antibody sequence - has resistance to e.g.  
 PT disrupting temperature, presence of proteolytic enzymes, etc.  
 XX  
 PS Example 2; Columns 27-30; 29pp; English.  
 XX The present sequence is a chimeric gene containing the cDNA for  
 CC the immunoglobulin (Ig) heavy and light chain variable regions of a  
 CC murine anti-asparaginase II monoclonal antibody (MAb), and human  
 CC asparaginase II. The gene was used in the preparation of a novel  
 CC recombinant chimeric polypeptide, comprising a 1st region  
 CC comprising a biologically active domain and another domain  
 CC containing an epitope, linked via a polypeptide to a 2nd region  
 CC including a single chain antibody (SCA) having the light and heavy  
 CC chains of an antibody variable region which specifically binds the  
 CC epitope in the 1st region. The chimeric polypeptide assumes a  
 CC conformation in which the SCA is bound to the epitope of the 1st  
 CC region and protects its biological activity from deactivation by  
 CC denaturing temperatures or pH conditions, proteolytic enzymes,  
 CC oxidising agents or alcohol. The regions of the chimeric  
 CC polypeptide interact to form a structure analogous to an  
 CC antibody-antigen complex. A D-asparaginase-SCA fusion protein of  
 CC the above type has better trypsin resistance than free  
 CC L-asparaginase.  
 XX  
 SQ Sequence 1848 BP; 435 A; 498 C; 517 G; 398 T; 0 other;  
 Query Match 37.4%; Score 343.6; DB 18; Length 1848;  
 Best Local Similarity 72.3%; Pred. No. 9,4e-78;  
 Matches 483; Conservative 0; Mismatches 164; Indels 21; Gaps 2;







GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 02:58:44 ; Search time 63 Seconds

(without alignments)  
6431.583 Million cell updates/sec

Title: US-08-657-449-13

Perfect score: 918 1 GAATTCATGAAAAAAGCCG.....ATCACCATTAGTGAAGCTT 918

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/prodata/2/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/prodata/2/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/prodata/2/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/prodata/2/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/prodata/2/ina/Backfillseq1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	3	US-08-862-124-13 Sequence 13, Appl
2	916.4	99.8	918	3	US-08-862-124-15 Sequence 15, Appl
3	799.6	87.1	867	3	US-08-862-124-16 Sequence 16, Appl
4	798	86.9	867	3	US-08-862-124-18 Sequence 18, Appl
5	361	39.3	450	3	US-08-862-124-6 Sequence 6, Appl
6	359.4	39.2	450	3	US-08-862-124-4 Sequence 4, Appl
7	345.2	37.6	783	4	US-08-487-283A-19 Sequence 19, Appl
8	343.6	37.4	1848	1	US-08-447-422-15 Sequence 15, Appl
9	324.4	35.3	543	3	US-08-862-124-3 Sequence 3, Appl
10	324.4	35.3	543	3	US-08-862-124-1 Sequence 1, Appl
11	318.4	34.7	4691	4	US-08-591-632-43 Sequence 43, Appl
12	318.4	34.7	4691	4	US-08-591-632-43 Sequence 43, Appl
13	318.4	34.7	6166	3	US-08-591-632-51 Sequence 51, Appl
14	318.4	34.7	6166	4	US-09-611-451-51 Sequence 51, Appl
15	303.6	33.1	1797	4	US-08-442-542-17 Sequence 17, Appl
16	303.6	33.1	1797	3	US-08-765-469-17 Sequence 17, Appl
17	300.6	32.7	752	6	5455030-12 Patent No. 5455030
18	289.4	31.5	402	1	US-08-405-034-3 Sequence 3, Appl
19	287.4	31.3	378	3	US-09-240-274-95 Sequence 95, Appl
20	287.2	31.3	723	1	US-07-988-430-92 Sequence 92, Appl
21	287.2	31.3	723	1	US-08-425-336-89 Sequence 89, Appl
22	287.2	31.3	723	1	US-08-488-113B-89 Sequence 89, Appl
23	287.2	31.3	723	1	US-08-477-484B-89 Sequence 89, Appl
24	287.2	31.3	723	2	US-08-646-360-89 Sequence 89, Appl
25	287.2	31.3	723	3	US-08-839-765-89 Sequence 89, Appl
26	287.2	31.3	723	3	US-09-136-389-89 Sequence 89, Appl
27	287.2	31.3	723	4	US-09-610-838-89 Sequence 89, Appl

28	287.2	31.3	723	5	PCT-US92-09487-92 Sequence 92, Appl
29	286	31.2	375	3	US-09-240-274-194 Sequence 194, Appl
30	284.2	31.0	378	3	US-09-240-274-94 Sequence 94, Appl
31	284.2	31.0	378	3	US-09-240-274-196 Sequence 196, Appl
32	283.8	30.9	784	2	US-08-956-047-32 Sequence 32, Appl
33	282.2	30.7	741	6	5455030-10 Patent No. 5455030
34	282	30.7	733	2	US-08-824-591-17 Sequence 17, Appl
35	281.2	30.6	900	1	US-08-926-789-17 Sequence 17, Appl
36	281.2	30.6	900	1	US-08-053-131-182 Sequence 182, Appl
37	281.2	30.6	900	1	US-08-096-762-182 Sequence 182, Appl
38	281.2	30.6	900	3	US-09-042-353-45 Sequence 45, Appl
39	281.2	30.6	900	4	US-08-758-417A-310 Sequence 310, Appl
40	281	30.6	369	4	US-09-560-198A-1 Sequence 1, Appl
41	281	30.6	378	3	US-09-240-274-195 Sequence 195, Appl
42	280.6	30.6	645	2	US-08-480-753-7 Sequence 7, Appl
43	278.2	30.3	646	1	US-08-300-386A-2 Sequence 2, Appl
44	278.2	30.3	646	3	US-08-931-645-2 Sequence 2, Appl
45	278.2	30.3	646	5	PCT-US94-01258-2 Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-08-862-124-13  
; Sequence 13, Application US/08862124  
; Patent No. 6207153  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; APPLICANT: Maitl, Pradip K.  
; APPLICANT: Kaplan, Howard A.  
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
; TITLE OF INVENTION: DETECTION OF CANCERS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster LLP  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/862,124  
; FILING DATE: 22-MAY-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lehnardt, Susan K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 31608-20001.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 918 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: join(1..906, 913..918)  
; US-08-862-124-13  
Query Match 100.0%; Score 918; DB 3; Length 918;  
Best Local Similarity 100.0%; Pred. No. 9,8e-252;

Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCCTATCGCATGCGATGCACTGCTGGTTTCCCTACCGTT 60  
DB 1 GAATTCATGAAAAAACCCTATCGCATGCGATGCACTGCTGGTTTCCCTACCGTT 60  
QY 61 GCGCAGGCGCATATGTTGTTGAGCAGCTCTCCAGGCAACCTGCTTTGTCTCCAGGGGAA 120  
DB 61 GCGCAGGCGCATATGTTGTTGAGCAGCTCTCCAGGCAACCTGCTTTGTCTCCAGGGGAA 120  
QY 121 AGAGCCACCTCTCTCTCCAGGCGCATGCAAGTGTATGAGCAGCTACTTACCTGTGTAC 180  
DB 121 AGAGCCACCTCTCTCTCCAGGCGCATGCAAGTGTATGAGCAGCTACTTACCTGTGTAC 180  
QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGCTGATCACCAGGGCCACT 240  
DB 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGCTGATCACCAGGGCCACT 240  
QY 241 GGCATGCGACAGGTTCACTGCGAGTGGGTCCGGGACAGACTTCACTCTCACCATCAGT 300  
DB 241 GGCATGCGACAGGTTCACTGCGAGTGGGTCCGGGACAGACTTCACTCTCACCATCAGT 300  
QY 301 AGACTGAGCCTGAGATTTTGCAGTATTAATCTGTCAGAGTATGTTAGTCACTCCTCAG 360  
DB 301 AGACTGAGCCTGAGATTTTGCAGTATTAATCTGTCAGAGTATGTTAGTCACTCCTCAG 360  
QY 361 ACACCTAGATCACTTTTGGCGGAGGAGCCAGGTGAGATCAAAACGACTGTGGCTGCA 420  
DB 361 ACACCTAGATCACTTTTGGCGGAGGAGCCAGGTGAGATCAAAACGACTGTGGCTGCA 420  
QY 421 CCATCTGCTCTGCGGCGGTTCCGGAGGTGTGATCAGGTGAGGTGGTCTCCAG 480  
DB 421 CCATCTGCTCTGCGGCGGTTCCGGAGGTGTGATCAGGTGAGGTGGTCTCCAG 480  
QY 481 GTGACGTGTGAGTCTGGGAGAGGCGTGTGTCAGCTGGAGGTCTCTGAGACTCTCC 540  
DB 481 GTGACGTGTGAGTCTGGGAGAGGCGTGTGTCAGCTGGAGGTCTCTGAGACTCTCC 540  
QY 541 TGTGACGCTCTGATTTCCCTTCAGAAAGCTTTTCTATGCACTGGGTCCGCAAGCTCTA 600  
DB 541 TGTGACGCTCTGATTTCCCTTCAGAAAGCTTTTCTATGCACTGGGTCCGCAAGCTCTA 600  
QY 601 GGCAGAGGCGTGGAGTGGGTGGAGTTATCATATGATGAGAGCACTAAATATCAAGCA 660  
DB 601 GGCAGAGGCGTGGAGTGGGTGGAGTTATCATATGATGAGAGCACTAAATATCAAGCA 660  
QY 661 GACTCCGTGAGAGGCGCATTCACCATCTCCAGAGCACTTCCAAAGAACCGGTGTATCTA 720  
DB 661 GACTCCGTGAGAGGCGCATTCACCATCTCCAGAGCACTTCCAAAGAACCGGTGTATCTA 720  
QY 721 AAAATGAAACGCTGAGAACTGAGAGACAGGCTGTCTATTACTGTGCGAGAGTCAAGC 780  
DB 721 AAAATGAAACGCTGAGAACTGAGAGACAGGCTGTCTATTACTGTGCGAGAGTCAAGC 780  
QY 781 CTGTTGGGTGACTATGACCACTACTACGTTTGAAGCTGTGGGCAAGAGGACCAAGCTC 840  
DB 781 CTGTTGGGTGACTATGACCACTACTACGTTTGAAGCTGTGGGCAAGAGGACCAAGCTC 840  
QY 841 ACCGTCTCTCAGAGATCCGAAACAAAACTGATCAGCGAAGAGATCTGAACCATCACCAT 900  
DB 841 ACCGTCTCTCAGAGATCCGAAACAAAACTGATCAGCGAAGAGATCTGAACCATCACCAT 900  
QY 901 CACCATTAAGTAAAGCTT 918  
DB 901 CACCATTAAGTAAAGCTT 918

RESULT 2  
US-08-862-124-15/C  
Sequence 15, Application US/08862124  
Patent No. 6207153  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.

APPLICANT: Maiti, Pradip K.  
APPLICANT: Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT  
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
TITLE OF INVENTION: DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/862,124  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 918 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-862-124-15

Query Match 99.8%; Score 916.4; DB 3; Length 918;  
Best Local Similarity 99.9%; Pred. No. 2.8e-251;  
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCCTATCGCATGCGATGCACTGCTGGTTTCCCTACCGTT 60  
DB 918 GAATTCATGAAAAAACCCTATCGCATGCGATGCACTGCTGGTTTCCCTACCGTT 859  
QY 61 GCGCAGGCGCATATGTTGTTGAGCAGCTCTCCAGGCAACCTGCTTTGTCTCCAGGGGAA 120  
DB 858 GCGCAGGCGCATATGTTGTTGAGCAGCTCTCCAGGCAACCTGCTTTGTCTCCAGGGGAA 799  
QY 121 AGAGCCACCTCTCTCTCCAGGCGCATGCAAGTGTATGAGCAGCTACTTACCTGTGTAC 180  
DB 121 AGAGCCACCTCTCTCTCCAGGCGCATGCAAGTGTATGAGCAGCTACTTACCTGTGTAC 180  
QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGCTGATCACCAGGGCCACT 240  
DB 798 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGCTGATCACCAGGGCCACT 679  
QY 241 GGCATGCGACAGGTTCACTGCGAGTGGGTCCGGGACAGACTTCACTCTCACCATCAGT 300  
DB 678 GGCATGCGACAGGTTCACTGCGAGTGGGTCCGGGACAGACTTCACTCTCACCATCAGT 300  
QY 301 AGACTGAGCCTGAGATTTTGCAGTATTAATCTGTCAGAGTATGTTAGTCACTCCTCAG 360  
DB 618 AGACTGAGCCTGAGATTTTGCAGTATTAATCTGTCAGAGTATGTTAGTCACTCCTCAG 360  
QY 361 ACACCTAGATCACTTTTGGCGGAGGAGCCAGGTGAGATCAAAACGACTGTGGCTGCA 420  
DB 558 ACACCTAGATCACTTTTGGCGGAGGAGCCAGGTGAGATCAAAACGACTGTGGCTGCA 499  
QY 421 CCATCTGCTCTGCGGCGGTTCCGGAGGTGTGATCAGGTGAGGTGGTCTCCAG 480





1 APPLICATION NUMBER: US/08/862,124  
2 FILING DATE: 22-MAY-1997  
3 CLASSIFICATION: 424  
4 ATTORNEY/AGENT INFORMATION:  
5 NAME: Lehnhardt, Susan K.  
6 REGISTRATION NUMBER: 33,943  
7 REFERENCE/DOCKET NUMBER: 31608-20001.20  
8 TELECOMMUNICATION INFORMATION:  
9 TELEPHONE: (650) 813-5600  
10 TELEFAX: (650) 494-0792  
11 TELEX: 706141  
12 INFORMATION FOR SEQ ID NO: 6:  
13 SEQUENCE CHARACTERISTICS:  
14 LENGTH: 450 base pairs  
15 TYPE: nucleic acid  
16 STRANDEDNESS: double  
17 TOPOLOGY: linear  
18 JS-08-862-124-6

Query Match	39.34;	Score 361;	DB 3;	Length 450;
Best Local Similarity	100.04;	Pred. No. 2.4e-93;		
Matches 361;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Oy	70	GATATTGTGTAACGCAAGTCTCCAGGCAACCCGTCTTTGTCTCCAGGGGAAAGACACC	122
Db	378	GATATTGTGTAACGCAAGTCTCCAGGCAACCCGTCTTTGTCTCCAGGGGAAAGACACC	319
Oy	130	CTCTCTCGACGGCCAGTCAGAGTGTTAAGACGTACTTAGCCCTGATACAGCAAA	189
Db	318	CTCTCTCGACGGCCAGTCAGAGTGTTAAGACGTACTTAGCCCTGATACAGCAAA	258
Oy	190	CTTGCCCAAGGCTCCCAAGCTCCTCAATCTAATGTGCAATCCACAGGGCCAATTGGCATGCCA	244
Db	258	CTTGCCCAAGGCTCCCAAGGCTCCTCAATCTAATGTGCAATCCACAGGGCCAATTGGCATGCCA	199
Oy	250	GACAGGTTCAAGTGGCAAGTGAGGTCCGGGACAGACTTCACTCTCAACATCAGTAGACTGGAG	308
Db	198	GACAGGTTCAAGTGGCAAGTGAGGTCCGGGACAGACTTCACTCTCAACATCAGTAGACTGGAG	135
Oy	310	CCTGAAGATTTTSCAGTGTATTAATCTGTACAGATATGTAAGCTCACTCAAGACCTTAG	365
Db	138	CCTGAAGATTTTSCAGTGTATTAATCTGTACAGATATGTAAGCTCACTCAAGACCTTAG	79
Oy	370	ATCACTTTCCGCGGAGGAGCAAGGTGGAGATCAACGAACTGTGGCTGCACATCTGTC	422
Db	78	ATCACTTTCCGCGGAGGAGCAAGGTGGAGATCAACGAACTGTGGCTGCACATCTGTC	19
Oy	430	T	430
Db	18	T	18

```

RESULT 6
US-08-862-124-4
; Sequence 4, Application US/08862124
; Patent No. 6207153
;
; GENERAL INFORMATION:
;
; APPLICANT: Dan, Michael D.
; APPLICANT: Maltz, Pradipt K.
; APPLICANT: Kaplan, Howard A.
;
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT
;
; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
;
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
;
; TITLE OF INVENTION: DETECTION OF CANCERS
;
; NUMBER OF SEQUENCES: 28
;
; CORRESPONDENCE ADDRESS:
;

```

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.304
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..450

```

Query Match	39.2%	Score 359.4;	DB 3;	Length 450;
Best Local Similarity	99.7%	Pred. No. 6.8e-93;		
Matches 360;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	70	GATATTGTTGACCGCAGTCTCCAGGACCCCTGTCTTTGTCTCCAGGGGAAAGCCACC	129
Db	73	GATATTGTTGACCGCAGTCTCCAGGACCCCTGTCTTTGTCTCCAGGGGAAAGCCACC	132
QY	130	CTCTCTCCAGAGGCCAGTCAGAGTGTTAGTAGCAGTACTTTCCTGGTATCCAGCGAAA	189
Db	133	CTCTCTCCAGAGGCCAGTCAGAGTGTTAGTAGCAGTACTTTCCTGGTATCCAGCGAAA	192
QY	190	CTGGGCCAGGCTCCGAGGCTCCTCATATGATGATCCAGAGGGCAGCTGGCATGCCA	249
Db	193	CTGGGCCAGGCTCCGAGGCTCCTCATATGATGATCCAGAGGGCAGCTGGCATGCCA	252
QY	250	GACAGGTTCAGTGAGTGGGTCCGGGACAGACTTCACCTCCACCATCAGTAGACTGGAG	309
Db	253	GACAGGTTCAGTGAGTGGGTCCGGGACAGACTTCACCTCCACCATCAGTAGACTGGAG	312
QY	310	CCTGAAGATTTTGCAGTGTATTACTGTACAGAGTATGTAGTCACTTCAGACACTCAG	369
Db	313	CCTGAAGATTTTGCAGTGTATTACTGTAGCAGTATGTAGTCACTTCAGACACTCAG	372
QY	370	ATCACTTTCCGGCGAGGGACCAAGGTGAGATCAACGAACTGTGGCTGCACATCTGTTC	429
Db	373	ATCACTTTCCGGCGAGGGACCAAGGTGAGATCAACGAACTGTGGCTGCACATCTGTTC	432
QY	430	T 430	
Db	433	T 433	

RESULT 7  
US-08-487-283A-19  
Sequence 19, Application US/08477283A  
Patent No. 6355245  
GENERAL INFORMATION:  
APPLICANT: Evans, Mark J.  
APPLICANT: Matlis, Louis A.  
APPLICANT: Mueller, Eileen Elliott  
APPLICANT: Nye, Steven H.  
APPLICANT: Rollins, Scott  
APPLICANT: Rothen, Russell P.  
APPLICANT: Springfield, Jeremy P.  
APPLICANT: Squinto, Stephen P.

APPLICANT: Thomas, Thomas C.  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT  
 OF INFLAMMATORY DISEASES  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Seth A. Fidel  
 STREET: 25 Science Park (Alexion)  
 CITY: New Haven  
 STATE: Connecticut  
 COUNTRY: USA  
 ZIP: 06511  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.4mb storage  
 OPERATING SYSTEM: System 7  
 SOFTWARE: WordPerfect 3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/487,283A  
 FILING DATE: June 7, 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/236,208  
 FILING DATE: 02-MAY-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seth A. Fidel  
 REGISTRATION NUMBER: 38,449  
 REFERENCE/DOCKET NUMBER: ALX-152.1 CIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (203) 776-1790  
 TELEFAX: (203) 772-3655  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 783 base pairs  
 TYPE: Nucleic Acid  
 STRANDEDNESS: Double  
 TOPOLOGY: linear  
 MOLECULE TYPE: Other nucleic acid  
 DESCRIPTION: N19/8 scFv (His Tagged)  
 US-08-487-283A-19

Query Match 37.6%; Score 345.2; DB 4; Length 783;  
 Best Local Similarity 69.3%; Pred. No. 9.5e-89;  
 Matches 552; Conservative 0; Mismatches 193; Indels 51; Gaps 4;

QY 66 GGGCGATATGTTGTTGACGAGTCCAGGCACTCTTGTCTCCAGGGGAAAGAC 125  
 DB 3 GGGCAATATGTTGTTGACGAGTCCAGGCACTCTTGTCTCCAGGGGAGAGGC 62  
 QY 126 CACCTCTCTGCGAGGGGCACTGAGGTAGT-----CAGCTACTAGGCTG 176  
 DB 63 CACCATATCTGCGAGGCACTGAGGTAGT-----CAGCTACTAGGCTG 122  
 QY 177 GTACAGAGAAACCTGCGAGGCTCCAGGCTCTCATCTATGATGATCCACAGGCG 236  
 DB 123 GTACAGAGAAACCTGCGAGGCTCCAGGCTCTCATCTATGATGATCCACAGGCG 182  
 QY 237 CATTGCGATGCGAGAGGCTGATGCGAGGTGGGCGGAGCACTTCACTTCACCAT 296  
 DB 183 ATCTGGGGTCCCTGCGAGGCTGATGCGAGGTGGGCGGAGCACTTCACTTCACCAT 242  
 QY 297 CAGTAGAGTGAAGCTGAAATTTTGCAGTATTAAGTGAAGAGTATGATGATCACC 356  
 DB 243 TGATCTGTGAGAGGTGATGATGCTGCACTTATTAAGTGAAGAGTATGATGATCACC 290  
 QY 357 TCAGAGAGCTGAGATCACTTTCGCGAGGAGCAAGGTGAGATCAAAAGCACTGTGGC 416  
 DB 291 TAAATGAGGTTCGAGAGCTTTCGCGAGGAGCAAGGTGAGATCAAAAGCACTGTGGC 343  
 QY 417 TGACCATCTGTCTGTGCGGCTGCGAGGTTCGAGAGGTGATGATGATGATGATGAT 476  
 DB 344 -----CCGAGGTGCGGCTGCGAGGTTCGAGAGGTGATGATGATGATGATGATGAT 389  
 QY 477 CAGGTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 536

DB 390 GAGAGCTGAGCTGCTGAGAGCTGCTGAGAGAGTATGAGAGCTTGGAGGCTCCCTGAACT 449  
 QY 537 CTCTGTGAGAGCTCTGAGATTCCTCCCTTCAAGAGCTTGTCTATGAGTCTGAGGCTCCGACAGC 596  
 DB 450 CTCTGTGAGAGCTCTGAGATTCCTCCCTTCAAGAGCTTGTCTATGAGTCTGAGGCTCCGACAGT 509  
 QY 597 TCTAGGCAAGGGGCTGAGTGGGTGGCACTTATATATATATATATATATATATATATATATATATATAT 656  
 DB 510 TCTAGGCAAGGGGCTGAGTGGGTGGCACTTATATATATATATATATATATATATATATATATATATAT 569  
 QY 657 CGCAGACTCCGTGAGAGGCGCATTCACATCTCCAGAGACACTTCCAGAAACCGGTGTA 716  
 DB 570 TCCAGACACTGTGAGAGGCGCATTCACATCTCCAGAGACAAATGCCAAGACACCTGTGA 629  
 QY 717 TCTAAATATGAGACGCTTGAAGACTGAGAGACAGGCTGTCTATATATATATATATATATATATATATAT 776  
 DB 630 TCTGCAAAATGAGAGCTGAGTGAAGCTGAGAGACAGGCTGTCTATATATATATATATATATATATATATAT 686  
 QY 777 GAGCTGTTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 836  
 DB 687 -----GACTTATTAAGAGGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 740  
 QY 837 GGTACCGTCTCTCTCA 852  
 DB 741 GGTACCGTCTCTCTCA 756

RESULT 8  
 US-08-447-422-15  
 Sequence 15, Application US/08447422  
 Patent No. 5686579  
 GENERAL INFORMATION:  
 APPLICANT: SHAMI, Ezekiel Y.  
 APPLICANT: ROTHSTEIN, Aser  
 APPLICANT: RAMJESINGH, Monabir  
 TITLE OF INVENTION: Use of Antibody/Antigen Interactions To  
 TITLE OF INVENTION: Protect or Modulate Biological Activity  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington, D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/447,422  
 FILING DATE:  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/081,410  
 FILING DATE: 22-JUN-1993  
 APPLICATION NUMBER: US 07/938,505  
 FILING DATE: 31-AUG-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/205,748  
 FILING DATE: 21-JUN-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BENT, Stephen A.  
 REGISTRATION NUMBER: 29,768  
 REFERENCE/DOCKET NUMBER: 17923/102 HYLI  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 672-5300  
 TELEFAX: (202) 672-5399  
 TELTEX: 904136  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1848 base pairs



TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-447-422-15

Query Match 37.4%; Score 343.6; DB 1; Length 1848;  
Best Local Similarity 72.3%; Pred. No. 3,9e-88;  
Matches 483; Conservative 0; Mismatches 164; Indels 21; Gaps 2;

```

QY 70 GATATGTGTGACGAGTCTCCAGGACCCCTGTTGCTCCAGGGGAAAGGCACC 129
DB 1 GATATGTGTGACGAGTCTCCAGGACCCCTGTTGCTCCAGGGGAAAGGCACC 60
QY 130 CTCTCCGAGGAGCCAGTGAAGTGTAGAGAGCTTACTGACCTGTGACAGAGAA 189
DB 61 ATGACCTGAGGGCCAGCTCAAGTGAATTCAGTTACTGACCTGTGACAGAGAA 120
QY 190 CTGCGCAGAGCTCCAGGCTCTCATCTATGTGTGATCCACAGGGCCACTGGCATGCA 249
DB 121 TCAGGTGCTCCCGCAAACTCTGAGATTATAGCACTCCAACTTGCTGTGAGTCCCT 180
QY 250 GACAGGTTGAGTGGCAGTGGGTCCGGGACAGACTTCACTCTGACCTGAGTGAAGTGG 309
DB 181 GCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCAATTCAGAGTGGAG 240
QY 310 CCTGAAGATTTTGCAGTGTATTAAGTGTGACAGTATGAGTCACTGACAGACCTCAG 369
DB 241 GCTGAAGATGCTGCCACTTATTACTGCCAGAGTACAGTGTATCCAC----- 289
QY 370 ATCACTTTGGCGAGGAGGACCAAGTGAATCAAGAACTGTGGCTGCACCATCTG-- 427
DB 290 -TCAGGTTGAGGGGGGACCAAGCTGGAATAAAGCGAGCTGATGCTGCACCACTGTA 348
QY 428 -----TCTGAGGCGGTGGCGGTTCCGAGGTGAGTCAAGTGGAGTGGTCCGAG 480
DB 349 TCCATCTTCCAGGTGGCGGTGGCTGGCGGTGGGTGGGTGGCGGTGGGTGGGTGGGT 408
QY 481 GTGCACTGTGTGAGTCTGGGGGAGCGGTGTGCAAGCTGGAGGTCCTGAGACTCTCC 540
DB 409 GTCAAGCTGTGAGAGTCTGGGGGAGCGGTGTGCAAGCTGGAGGTCCTGAGACTCTCC 468
QY 541 TGTGCACTGTGAGTCTGGGGGAGCGGTGTGCAAGCTGGAGGTCCTGAGACTCTCC 600
DB 469 TGTGCACTGTGAGTCTGGGGGAGCGGTGTGCAAGCTGGAGGTCCTGAGACTCTCC 528
QY 601 GGCAAGGGGCTGAGTGGGTGCAAGTGTATGATGATGAGAGCACTAAATATATGCA 660
DB 529 GGAAGGGGCTGAGTGGGTGCAAGTGTATGATGAGAGCACTAAATATATGCA 588
QY 661 GACTCCGTAAGGGCGATTCACATCTCCAGAGACATTCAGAGAGCGGTATCTA 720
DB 589 GACACAGTGAAGGGCGATTCACATCTCCAGAGACATTCAGAGAGCGGTATCTA 648
QY 721 AAAATGAA 728
DB 649 CAATGAA 656

```

RESULT 9  
US-08-862-124-1  
Sequence 1, Application US/08862124  
Patent No. 6207153  
GENERAL INFORMATION:

APPLICANT: Dan, Michael D.  
APPLICANT: Maiti, Pradip K.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP

STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/862,124  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 543 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..543  
US-08-862-124-1

Query Match 35.3%; Score 324.4; DB 3; Length 543;  
Best Local Similarity 89.3%; Pred. No. 6.7e-83;  
Matches 349; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

```

QY 440 GCGGTTCCGAGAGTGTGATGATGAGTGGGTGCGGAGGTCAGGCTGTGAGTCTG 499
DB 152 GGGTTTCTCTGCTGCTCTTTTAAGAGTATCAAGTGTGAGTGGTGTGAGTCTG 211
QY 500 GGGGAGGCGTGTGTCAGGCTGGGAGGTCCTGAGACTCTCTGTGAGCTGTGATTC 559
DB 212 GGGGAGGCGTGTGTCAGGCTGGGAGGTCCTGAGACTCTCTGTGAGCTGTGATTC 271
QY 560 CTTTGAAGCTTTGCTATGCACTGGGTCCGCAAGCTCTTGAAGGAGGCTGTGAGTGG 619
DB 272 CTTTGAAGCTTTGCTATGCACTGGGTCCGCAAGCTCTTGAAGGAGGCTGTGAGTGG 331
QY 620 TGGGAGTATATCATATGATGAGAGCACTAAATATGAGCAAGTCCGTAAGGGCCGAT 679
DB 332 TGGGAGTATATCATATGATGAGAGCACTAAATATGAGCAAGTCCGTAAGGGCCGAT 391
QY 680 TCACCATCTCCAGAGACATTCAGAGAACACGCTGTATCTAAATATGAGCAAGCTGAGAA 739
DB 392 TCACCATCTCCAGAGACATTCAGAGAACACGCTGTATCTAAATATGAGCAAGCTGAGAA 451
QY 740 CTGAGGACAGGCTGTCTATTAAGTGTGAGAGATCAAGAGCTGTGGTGAATGACC 799
DB 452 CTGAGGACAGGCTGTCTATTAAGTGTGAGAGATCAAGAGCTGTGGTGAATGACC 511
QY 800 ACTACTACGGTTTGGAGCGTGGGCAAGG 830
DB 512 ACTACTACGGTTTGGAGCGTGGGCAAGG 542

```

RESULT 10  
US-08-862-124-3/C  
Sequence 3, Application US/08862124  
Patent No. 6207153  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
APPLICANT: Maiti, Pradip K.

? APPLICANT: Kaplan, Howard A.  
 ? TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
 ? SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
 ? TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
 ? TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
 ? TITLE OF INVENTION: DETECTION OF CANCERS  
 ? NUMBER OF SEQUENCES: 28  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Morrison & Foerster LLP  
 ? STREET: 755 Page Mill Road  
 ? CITY: Palo Alto  
 ? STATE: CA  
 ? COUNTRY: USA  
 ? ZIP: 94304-1018  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/862,124  
 ? FILING DATE: 22-MAY-1997  
 ? CLASSIFICATION: 424  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: lehnardt, Susan K.  
 ? REGISTRATION NUMBER: 33,943  
 ? REFERENCE/DOCKET NUMBER: 31608-20001.20  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: (650) 813-5600  
 ? TELEFAX: (650) 494-0792  
 ? TELEX: 706141  
 ? INFORMATION FOR SEQ ID NO: 3:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 543 base pairs  
 ? TYPE: nucleic acid  
 ? STRANDEDNESS: double  
 ? TOPOLOGY: linear  
 ? US-08-862-124-3



ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 332.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937  
TELEFAX: (619) 784-9399  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6166 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
US-08-591-632-51

Query Match 34.7%; Score 318.4; DB 3; Length 6166;  
Best Local Similarity 88.4%; Pred. No. 9,7e-81;  
Matches 375; Conservative 0; Mismatches 31; Indels 18; Gaps 2;

QY 7 ATGAAAAAACCGCTATGCGGATCGCATGTCATGCTGGCTGGTTGCTTACCGTTGCGGAG 66  
DB 4541 ATGAAAAAGACAGCTATGCGGATCGCATGTCATGCTGGCTGGTTGCTTACCGTTGCGGAG 4600  
QY 67 GCCGATATTTGTTGACGAGTCTCCAGGACACCTGCTTTGCTCCAGGGGAAAGAGCC 126  
DB 4601 GCGG---CCGAGCTCAGCGAGTCTCCAGGACACCTGCTTTGCTCCAGGGGAAAGAGCC 4657  
QY 127 ACCCTCTCTGCGAGGCGCATGTCAGAGTGTAGTACACCTTACCTTGTGTTACCGAGAG 186  
DB 4658 ACCCTCTCTGCGAGGCGCATGTCAGAGTGTAGTACACCTTACCTTGTGTTACCGAGAG 4717  
QY 187 AAACCTGGCCAGGCTCCAGGCTCCTCATCTATGTTGATCCACAGGGGCCACTGGGCA 246  
DB 4718 AAACCTGGCCAGGCTCCAGGCTCCTCATCTATGTTGATCCACAGGGGCCACTGGGCA 4777  
QY 247 CCAGACAGGTTCAGTGGAGTGGTCCGGGACAGACTTCACTTCACTCCATCAGTAGACTG 306  
DB 4778 CCAGACAGGTTCAGTGGAGTGGTCCGGGACAGACTTCACTTCACTCCATCAGTAGACTG 4837  
QY 307 GAGCTGGAAGATTTTGCAGTGTATTAATCTGTACAGCATGTGTAGTCTCACTCCATCAGACT 366  
DB 4838 GAGCTGGAAGATTTTGCAGTGTATTAATCTGTACAGCATGTGTAGTCTCACTCCATCAGACT 4891  
QY 367 CAGATCACTTTCGGCGAGGAGCCAAAGGTGAGATCAAAAGCACTGTGGTGCACCATCT 426  
DB 4892 -----TTGGCCAAAGGAGCCAAAGGTGAGATCAAAAGCACTGTGGTGCACCATCT 4942  
QY 427 GTCT 430  
DB 4943 GTCT 4946

RESULT 14  
US-09-611-451-51  
Sequence 51, Application US/09611451  
Patent No. 6395275  
GENERAL INFORMATION:  
APPLICANT: Burbas, Carlos F.  
Lerner, Rignard A.  
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL  
ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
Patent Counsel  
STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/611,451  
FILING DATE: 06-Jul-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/591,632  
FILING DATE: 2001-10-29  
APPLICATION NUMBER: US 08/308,841  
FILING DATE: 19-SEP-1994  
APPLICATION NUMBER: US 08/233,619  
FILING DATE: 26-APR-1994  
APPLICATION NUMBER: US 08/139,409  
FILING DATE: 19-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 332.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937  
TELEFAX: (619) 784-9399  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6166 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-09-611-451-51

Query Match 34.7%; Score 318.4; DB 4; Length 6166;  
Best Local Similarity 88.4%; Pred. No. 9,7e-81;  
Matches 375; Conservative 0; Mismatches 31; Indels 18; Gaps 2;

QY 7 ATGAAAAAACCGCTATGCGGATCGCATGTCATGCTGGCTGGTTGCTTACCGTTGCGGAG 66  
DB 4541 ATGAAAAAGACAGCTATGCGGATCGCATGTCATGCTGGCTGGTTGCTTACCGTTGCGGAG 4600  
QY 67 GCCGATATTTGTTGACGAGTCTCCAGGACACCTGCTTTGCTCCAGGGGAAAGAGCC 126  
DB 4601 GCGG---CCGAGCTCAGCGAGTCTCCAGGACACCTGCTTTGCTCCAGGGGAAAGAGCC 4657  
QY 127 ACCCTCTCTGCGAGGCGCATGTCAGAGTGTAGTACACCTTACCTTGTGTTACCGAGAG 186  
DB 4658 ACCCTCTCTGCGAGGCGCATGTCAGAGTGTAGTACACCTTACCTTGTGTTACCGAGAG 4717  
QY 187 AAACCTGGCCAGGCTCCAGGCTCCTCATCTATGTTGATCCACAGGGGCCACTGGGCA 246  
DB 4718 AAACCTGGCCAGGCTCCAGGCTCCTCATCTATGTTGATCCACAGGGGCCACTGGGCA 4777  
QY 247 CCAGACAGGTTCAGTGGAGTGGTCCGGGACAGACTTCACTTCACTCCATCAGTAGACTG 306  
DB 4778 CCAGACAGGTTCAGTGGAGTGGTCCGGGACAGACTTCACTTCACTCCATCAGTAGACTG 4837  
QY 307 GAGCTGGAAGATTTTGCAGTGTATTAATCTGTACAGCATGTGTAGTCTCACTCCATCAGACT 366  
DB 4838 GAGCTGGAAGATTTTGCAGTGTATTAATCTGTACAGCATGTGTAGTCTCACTCCATCAGACT 4891  
QY 367 CAGATCACTTTCGGCGAGGAGCCAAAGGTGAGATCAAAAGCACTGTGGTGCACCATCT 426  
DB 4892 -----TTGGCCAAAGGAGCCAAAGGTGAGATCAAAAGCACTGTGGTGCACCATCT 4942  
QY 427 GTCT 430  
DB 4943 GTCT 4946

RESULT 15  
US-08-442-542-17  
Sequence 17, Application US/08442542

Patent No. 5686600  
GENERAL INFORMATION:  
APPLICANT: Carozzi, Nadine B.  
APPLICANT: Koziel, Michael G.  
TITLE OF INVENTION: Antibodies which Bind to Insect Gut  
TITLE OF INVENTION: Proteins and their Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ciba-Geigy Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: NY  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,542  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 530  
PRIORITY INFORMATION: 530  
APPLICATION NUMBER: US 08/267,641  
FILING DATE: 28-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Spull, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: OGC 1750  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8615  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1797 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1797  
OTHER INFORMATION: /note="381 single chain antibody"  
OTHER INFORMATION: from pc184631"  
US-08-442-542-17

Query Match 33.1%; Score 303.6; DB 1; length 1797;  
Best Local Similarity 68.7%; Pred. No. 9.3e-77;  
Matches 493; Conservative 0; Mismatches 189; Indels 36; Gaps 4;

QY 70 GATATTGTTGTCGAGTCTCCAGGACCCCTCTTTGTCGAGGGGAAAGGCCACC 129  
DB 67 GACATTGTGTCGACCGACGTCCTCTTGGCTGTCTTAGGGGAGAGGGCCACC 126  
QY 130 CTCTCTGAGGGGCGAGTCAGAGTGTAGT-----AGCAGTACTTACCTGCTAC 180  
DB 127 ATCTCTGAGAGCCAGCGAAAGTGTGATCATATGACATTAGTTTATGAACTGTTTC 186  
QY 181 CAGCAGAAACTGGCCAGGCTCCAGGCTCTCATCTATGTGTCATCCACAGGGCCACT 240  
DB 187 CAACAGAAACAGAGACAGCCAAACCTCATCTATGTGTCATCCAAAGGATCC 246  
QY 241 GGCATCCGAGAGGTCGAGTGTGTCAGTGGTCCGGGACAGACTTCACTGACATCAAT 300  
DB 247 GGGGTCTCCGAGGTTTAGTGGCAGTGGTCTGGGACAGACTTCACTGACATCAAT 306  
QY 301 AGACTGAGGCTGAGAGATTGTCAGTGTATTACTGTGACAGATGATGATCACTCAG 360  
DB 307 CCAATGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 354  
QY 361 ACACTGAGATCACTTTGGCGGAGGAGCCAGGTGAGATCAACGAACTGTGGCTGCA 420

DB 355 GAACCTCCGTACACGTTGCGAGGGGGACACCGCTGGAATTAAGGGGCTGATGCTGCA 414  
QY 421 CCATCTGTCTGTGCGCGGTGCGGCTTCGAGAGGTGATGATGAGTGGCTCCAG 480  
DB 415 CCACTGATGATGTTGGCGGTGCTGCGGCGGTGGTGGT-----GCTGAGCAG 465  
QY 481 GTGCACTGTGTGAGTCTGCGGGGAGCGGTGTCAGCTTGGGAGGTCCCTGAGACTCTCC 540  
DB 466 GTCAACTGCGAGAGTGTGTGAGGATTTGGCAGCCCTAAAGGCTCATTTGAACCTCTCA 525  
QY 541 TGTGAGCCTCTGGAATTCCTTCAGAACTTGTGATGACATGAGTCCGCGAGGCTCTTA 600  
DB 526 TGTGAGCCTCTGGAATTCCTTCAGAACTTGTGATGACATGAGTCCGCGAGGCTCTCA 585  
QY 601 GGCAGAGGCGTGGAGTGGTGGCAGTTATATGATGATGAGCA-----CTAAATAC 654  
DB 586 GGAAGGGTTTGAATGGTTGCTGTCATTAAGAAAGTAAATATATGATGACATCTC 645  
QY 655 TACGCACTCTCGTGAAGGCGGATTCATCATCTCCAGAGACACTTCCAAAGACAGGTG 714  
DB 646 TATGGGATTCAGTGAAAGACAGTTCAACCGTCTCCAGAGATGATTCACAAAGCATGTTTC 705  
QY 715 TATCTAAATATGAAACGCTGAGACTGAGACAGGCTGTCTATTACTGTGCGAGAG 772  
DB 706 TATCTGCAATGAACTTGAATGAGACAGCCATGTATTACTGTGTAGGG 763

Search completed: September 17, 2003, 04:23:14  
Job time : 68 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 03:49:20 ; Search time 871 Seconds  
(without alignments)  
2592.658 Million cell updates/sec

Title: US-08-657-449-13

Perfect score: 918  
Sequence: 1 GAATTCATCAAAAAACCGC.....ATCACCATTAAGTGAAGCTT 918

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 122959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	11	US-09-782-397-13 Sequence 13, Appl
2	916.4	99.8	918	11	US-09-782-397-15 Sequence 15, Appl
3	799.6	87.1	867	11	US-09-782-397-16 Sequence 16, Appl
4	798	86.9	867	11	US-09-782-397-18 Sequence 18, Appl
5	361	39.3	450	11	US-09-782-397-6 Sequence 6, Appl
6	359.4	39.2	450	11	US-09-782-397-4 Sequence 4, Appl
7	324.4	35.3	543	11	US-09-782-397-1 Sequence 1, Appl
8	324.4	35.3	543	11	US-09-782-397-3 Sequence 3, Appl
9	319.8	34.8	1413	14	US-10-153-382-16 Sequence 16, Appl
10	310.6	33.8	678	11	US-09-453-234-85 Sequence 85, Appl
11	310.6	33.8	678	11	US-09-453-234-49 Sequence 49, Appl
12	305.8	33.3	678	11	US-09-453-234-37 Sequence 37, Appl
13	305.8	33.3	678	11	US-09-453-234-41 Sequence 41, Appl
14	305.8	33.3	678	11	US-09-453-234-71 Sequence 71, Appl
15	303.8	33.1	379	12	US-10-041-860-59 Sequence 59, Appl
16	303.2	33.0	414	12	US-10-325-694-143 Sequence 143, App

17	302.6	33.0	678	11	US-09-453-234-73 Sequence 73, Appl
18	302.2	32.9	379	12	US-10-041-860-67 Sequence 67, Appl
19	301	32.8	678	11	US-09-453-234-79 Sequence 79, Appl
20	301	32.8	948	10	US-09-859-053-33 Sequence 33, Appl
21	300.2	32.7	672	11	US-09-453-234-51 Sequence 51, Appl
22	299.8	32.7	708	14	US-10-153-382-6 Sequence 6, Appl
23	299.4	32.6	970	10	US-09-859-053-37 Sequence 37, Appl
24	297	32.4	672	11	US-09-453-234-39 Sequence 39, Appl
25	297	32.4	672	11	US-09-453-234-75 Sequence 75, Appl
26	295.4	32.2	357	12	US-10-226-615-3 Sequence 3, Appl
27	295.4	32.2	672	11	US-09-453-234-43 Sequence 43, Appl
28	295.4	32.2	672	11	US-09-453-234-77 Sequence 77, Appl
29	295.2	32.2	367	12	US-10-330-613-31 Sequence 31, Appl
30	295.2	32.2	367	12	US-10-330-530-31 Sequence 13125, A
31	293.4	32.0	961	14	US-10-198-846-11125 Sequence 16641, A
32	292.8	31.9	413	11	US-09-918-995-16641 Sequence 16641, A
33	292	31.8	1184	14	US-10-158-646-60 Sequence 60, Appl
34	291.8	31.8	1458	14	US-10-158-646-66 Sequence 66, Appl
35	290.2	31.6	1775	14	US-10-158-646-64 Sequence 64, Appl
36	288.6	31.4	645	11	US-09-972-656-99 Sequence 99, Appl
37	287.4	31.3	378	11	US-09-848-798-95 Sequence 95, Appl
38	287.2	31.3	723	12	US-10-127-890-89 Sequence 89, Appl
39	287	31.3	645	11	US-09-791-153A-48 Sequence 48, Appl
40	286.8	31.2	1202	14	US-10-158-646-57 Sequence 57, Appl
41	286.4	31.2	382	12	US-10-041-860-75 Sequence 75, Appl
42	286	31.2	375	11	US-09-848-798-194 Sequence 194, App
43	285.2	31.1	1798	9	US-09-925-299-230 Sequence 230, App
44	285.2	31.1	1798	11	US-09-925-299-230 Sequence 94, Appl
45	284.2	31.0	378	11	US-09-848-798-94 Sequence 94, Appl

#### ALIGNMENTS

RESULT 1  
US-09-782-397-13  
Sequence 13, Application US/09782397  
Publication No. US20030021779A1  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
Mailli, Pradip K.  
Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Leinhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792

TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 918 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: join(1..906, 913..918)  
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
 US-09-782-397-13

Query Match 100.0%; Score 918; DB 11; Length 918;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-270; Mismatches 0; Gaps 0;  
 Matches 918; Conservative 0; Indels 0; Gaps 0;

```

QY 1 GAATTCATGAAAAAACCAGTATGCGATCGCATGCGATGCGATGCGTGGTTGCTACCGTT 60
DB 1 GAATTCATGAAAAAACCAGTATGCGATCGCATGCGATGCGATGCGTGGTTGCTACCGTT 60
QY 61 GCGCAGGCCGATATGTTGTTGACGCACTCTCCAGGACCCCTGCTTGTCTCCAGGGAA 120
DB 61 GCGCAGGCCGATATGTTGTTGACGCACTCTCCAGGACCCCTGCTTGTCTCCAGGGAA 120
QY 121 AGAGCCACCTCTCTCTGAGGGGCGACGTCAGAGTTAGTACAGCTACTTACCTGGTAC 180
DB 121 AGAGCCACCTCTCTCTGAGGGGCGACGTCAGAGTTAGTACAGCTACTTACCTGGTAC 180
QY 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCCTCATCTATGTTGATCCACAGGGCCACT 240
DB 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCCTCATCTATGTTGATCCACAGGGCCACT 240
QY 241 GGCATGCGCAGCAGGTTGAGGAGTGAGTGGTCCGGGACAGCTTCACTCTCAACATCA 300
DB 241 GGCATGCGCAGCAGGTTGAGGAGTGAGTGGTCCGGGACAGCTTCACTCTCAACATCA 300
QY 301 AGATGAGGCTGGAAGATTTTGGCATGATATCTGTCAGCATGATGATGATGATGATGAT 360
DB 301 AGATGAGGCTGGAAGATTTTGGCATGATATCTGTCAGCATGATGATGATGATGATGAT 360
QY 361 ACACCTCAGATCACTTTCGGGCGAGGAGCAAGGTGAGATCAACAGAACTGTGGCTCA 420
DB 361 ACACCTCAGATCACTTTCGGGCGAGGAGCAAGGTGAGATCAACAGAACTGTGGCTCA 420
QY 421 CCATCTGCTCTGCGGCGTGGCGGTTCCGAGAGTGTGATCAAGTGAAGTGGCTCCAG 480
DB 421 CCATCTGCTCTGCGGCGTGGCGGTTCCGAGAGTGTGATCAAGTGAAGTGGCTCCAG 480
QY 481 GTGACGCTGTGAGTCTGGGCGAGGAGGCTGTCAGGCTCGAGAGGCTCCAGACTCC 540
DB 481 GTGACGCTGTGAGTCTGGGCGAGGAGGCTGTCAGGCTCGAGAGGCTCCAGACTCC 540
QY 541 TGTGACGCTGTGAGTCTGGGCGAGGAGGCTGTCAGGCTCGAGAGGCTCCAGACTCC 600
DB 541 TGTGACGCTGTGAGTCTGGGCGAGGAGGCTGTCAGGCTCGAGAGGCTCCAGACTCC 600
QY 601 GGCAGAGGGGCTGAGTGGGCTGAGTATATATATATATATATATATATATATATATAT 660
DB 601 GGCAGAGGGGCTGAGTGGGCTGAGTATATATATATATATATATATATATATATATAT 660
QY 661 GACTCCGCTGAGAGGCGGCTTCAACCTCTCCAGAGCACTTCCAGAAACAAGCTGTAT 720
DB 661 GACTCCGCTGAGAGGCGGCTTCAACCTCTCCAGAGCACTTCCAGAAACAAGCTGTAT 720
QY 721 AAAATGACAGGCTGAGAGGAGGAGCAGGCTGCTATTAATCTGCGAGAGATCAGAGC 780
DB 721 AAAATGACAGGCTGAGAGGAGGAGCAGGCTGCTATTAATCTGCGAGAGATCAGAGC 780
QY 781 CTGTTGGGTGACTATGACCACTACTACGTTTGAAGCTCTGCGGCAAAAGGACCAAGCTC 840
DB 781 CTGTTGGGTGACTATGACCACTACTACGTTTGAAGCTCTGCGGCAAAAGGACCAAGCTC 840
  
```

QY 841 ACCGTCCTCGAGATCCGACAAAAAGTATGAGGAGAGATCTGAACATCAACAT 900  
 DB 841 ACCGTCCTCGAGATCCGACAAAAAGTATGAGGAGAGATCTGAACATCAACAT 900  
 QY 901 CACCATTAAGTGAAGCTT 918  
 DB 901 CACCATTAAGTGAAGCTT 918

RESULT 2  
 US-09-782-397-15/c  
 Sequence 15, Application US/09782397  
 Publication No. US20030021779A1  
 GENERAL INFORMATION:  
 APPLICANT: Dan, Michael D.  
 Maiti, Pradip K.  
 Kaplan, Howard A.  
 TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS

NUMBER OF SEQUENCES: 28  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Morrison & Foerster LLP  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304-1018

COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/782,397  
 FILING DATE: 13-Feb-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/662,124  
 FILING DATE: 1997-05-22

ATTORNEY/AGENT INFORMATION:  
 NAME: Lehnhardt, Susan K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 31608-20001.20

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 813-5600  
 TELEFAX: (650) 494-0792  
 TELEX: 706141

INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 918 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
 US-09-782-397-15

Query Match 99.8%; Score 916.4; DB 11; Length 918;  
 Best Local Similarity 99.9%; Pred. No. 2.4e-269; Mismatches 1; Indels 0; Gaps 0;  
 Matches 917; Conservative 0; Indels 0; Gaps 0;

```

QY 1 GAATTCATGAAAAAACCAGTATGCGATGCGATGCGATGCGTGGTTGCTACCGTT 60
DB 1 GAATTCATGAAAAAACCAGTATGCGATGCGATGCGATGCGTGGTTGCTACCGTT 859
QY 61 GCGCAGGCCGATATGTTGTTGACGCACTCTCCAGGACCCCTGCTTGTCTCCAGGGAA 120
DB 61 GCGCAGGCCGATATGTTGTTGACGCACTCTCCAGGACCCCTGCTTGTCTCCAGGGAA 799
QY 121 AGAGCCACCTCTCTCTGAGGGGCGACGTCAGAGTTAGTACAGCTACTTACCTGGTAC 180
DB 121 AGAGCCACCTCTCTCTGAGGGGCGACGTCAGAGTTAGTACAGCTACTTACCTGGTAC 739
  
```



QY 181 CAGCAGAACTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACGAGGCTACT 240  
DB 738 CAGCAGAACTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACGAGGCTACT 679  
QY 241 GGCATGCCGAGACGGTTCAGTGGGATCCCGGACAGACTTCCTCAGCAGTACT 300  
DB 678 GGCATGCCGAGACGGTTCAGTGGGATCCCGGACAGACTTCCTCAGCAGTACT 619  
QY 301 AGACTGAGCCTGAGATTTTTCAGTGTATTAATCTGTCAGAGATGATGATCAGCTCAG 360  
DB 618 AGACTGAGCCTGAGATTTTTCAGTGTATTAATCTGTCAGAGATGATGATCAGCTCAG 559  
QY 361 ACACCTCAGATCACTTTCGCGGAGGAGCCAGAGTGAATCAACGAACTGTGGCTGCA 420  
DB 558 ACACCTCAGATCACTTTCGCGGAGGAGCCAGAGTGAATCAACGAACTGTGGCTGCA 499  
QY 421 CCATCTGTCTCTGGCGGCTGGCGGCTTCGAGAGTGTGATCAGAGTGAAGTGGCTCCAG 480  
DB 498 CCATCTGTCTCTGGCGGCTGGCGGCTTCGAGAGTGTGATCAGAGTGAAGTGGCTCCAG 439  
QY 481 GTGCACTGGTGAAGTCTGGGAGGAGGCTGTGCTCAGGCTGGAGGCTCCGAGACTTCC 540  
DB 438 GTGCACTGGTGAAGTCTGGGAGGAGGCTGTGCTCAGGCTGGAGGCTCCGAGACTTCC 379  
QY 541 TGTGAGCCTCTGATTTCCCTTTCAGAACTTGTGATGATGATGATGATGATGATGAT 600  
DB 378 TGTGAGCCTCTGATTTCCCTTTCAGAACTTGTGATGATGATGATGATGATGATGAT 319  
QY 601 GGCAGAGGCTGAGAGTGGTGGGATTTATCATATGATGAGACACTAAATATCTAGCA 660  
DB 318 GGCAGAGGCTGAGAGTGGTGGGATTTATCATATGATGAGACACTAAATATCTAGCA 259  
QY 661 GACTCCGTGAAGGCGGATTCACCATCTCCAGAGACACTTCCAGAAACCGGTATCTA 720  
DB 258 GACTCCGTGAAGGCGGATTCACCATCTCCAGAGACACTTCCAGAAACCGGTATCTA 199  
QY 721 AAAATGACAGCCTGAGAACTGAGACACGCGTGTCTATTAATCTGTCAGAGATCAGAGC 780  
DB 198 AAAATGACAGCCTGAGAACTGAGACACGCGTGTCTATTAATCTGTCAGAGATCAGAGC 139  
QY 781 CTGTTGGTGAATCACTAATCACTAATCACTAATCACTAATCACTAATCACTAATCACT 840  
DB 138 CTGTTGGTGAATCACTAATCACTAATCACTAATCACTAATCACTAATCACTAATCACT 79  
QY 841 ACCGTCTCTCAGGATCCGAGAACTGATGAGGAGAGATCTGAACTCATCACTCAT 900  
DB 78 ACCGTCTCTCAGGATCCGAGAACTGATGAGGAGAGATCTGAACTCATCACTCAT 19  
QY 901 CACCATTAAGTGAAGCTT 918  
DB 18 CACCATTAAGTGAAGCTT 1

RESULT 3  
US-09-782-397-16  
; Sequence 16, Application US/0782397  
; Publication No. US20030021779A1  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; Maiti, Pradip K.  
; Kaplan, Howard A.  
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT  
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
DETECTION OF CANCERS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
ADDRESS: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA

ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 867 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1..855, 862..867)  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-782-397-16

Query Match 87.1%; Score 799.6; DB 11; Length 867;  
Best Local Similarity 94.0%; Pred. No. 1e-233;  
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

QY 1 GAATTCATGAAAAAACCCTATTCGATGAGATGTCAGTGGCTGCTGCTACCGTT 60  
DB 1 GAATTCATGAAAAAACCCTATTCGATGAGATGTCAGTGGCTGCTGCTACCGTT 60  
QY 61 GGCAGAGCGGATATGTGTGAAGCATGCTCAGAGCACTCTGTTGTCTCCAGGGAA 120  
DB 61 GGCAGAGCGGATATGTGTGAAGCATGCTCAGAGCACTCTGTTGTCTCCAGGGAA 120  
QY 121 AAGGCCACCTCTCTGCGAGGCGCATGAGATGTTAGAGCAAGCTTAAGCTGTAC 180  
DB 61 GGCAGAGCGGATATGTGTGAAGCATGCTCAGAGCACTCTGTTGTCTCCAGGGAA 120  
QY 121 AAGGCCACCTCTCTGCGAGGCGCATGAGATGTTAGAGCAAGCTTAAGCTGTAC 180  
DB 121 AAGGCCACCTCTCTGCGAGGCGCATGAGATGTTAGAGCAAGCTTAAGCTGTAC 180  
QY 181 CAGCAGAACTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACGAGGCTACT 240  
DB 181 CAGCAGAACTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACGAGGCTACT 240  
QY 241 GGCATGCCGAGACGGTTCAGTGGGATCCCGGACAGACTTCCTCAGCAGTACT 300  
DB 241 GGCATGCCGAGACGGTTCAGTGGGATCCCGGACAGACTTCCTCAGCAGTACT 300  
QY 301 AGACTGAGCCTGAGATTTTTCAGTGTATTAATCTGTCAGAGATGATGATCAGCTCAG 360  
DB 301 AGACTGAGCCTGAGATTTTTCAGTGTATTAATCTGTCAGAGATGATGATCAGCTCAG 360  
QY 361 ACACCTCAGATCACTTTCGCGGAGGAGCCAGAGTGAATCAACGAACTGTGGCTGCA 420  
DB 361 ACACCTCAGATCACTTTCGCGGAGGAGCCAGAGTGAATCAACGAACTGTGGCTGCA 420  
QY 421 CCATCTGTCTCTGGCGGCTGGCGGCTTCGAGAGTGTGATCAGAGTGAAGTGGCTCCAG 480  
DB 421 TC-----CGAGCAG 429  
QY 481 GTGCACTGGTGAAGTCTGGGAGGAGGCTGTGCTCAGGCTGGAGAGTCCCTGAGACTTCC 540  
DB 430 GTGCACTGGTGAAGTCTGGGAGGAGGCTGTGCTCAGGCTGGAGAGTCCCTGAGACTTCC 489

```

QY 541 TGTGAGGCTCTGAGATTCCTCCCTTCAAGAGCTTTGCTATGCACTGGGTCGCGCAGGCTCTA 600
DB 490 TGTGAGGCTCTGAGATTCCTCCCTTCAAGAGCTTTGCTATGCACTGGGTCGCGCAGGCTCTA 549
QY 601 GGCAGAGGGGCTGAGTGGGTGGGTCAGTTATATCATATGATGAGACATAAATACACCA 660
DB 550 GGCAGAGGGGCTGAGTGGGTGGGTCAGTTATATCATATGATGAGACATAAATACACCA 609
QY 661 GACTCCGTGAGAGGGCCGATTCACATCTCCAGAGACACTTCCAGAGACAGGCTGTATCTA 720
DB 610 GACTCCGTGAGAGGGCCGATTCACATCTCCAGAGACACTTCCAGAGACAGGCTGTATCTA 669
QY 721 AAATGAGACAGGCTGAGACTGAGACACGCGTGTCTATTACTGTGGAGAGATGAGAC 780
DB 670 AAATGAGACAGGCTGAGACTGAGACACGCGTGTCTATTACTGTGGAGAGATGAGAC 729
QY 781 CTGTTGGGTGACTATGACCACTACTACGTTTGAAGCTGTGGGCAAGGACACGCTC 840
DB 730 CTGTTGGGTGACTATGACCACTACTACGTTTGAAGCTGTGGGCAAGGACACGCTC 789
QY 841 ACCGTCTCTCAGAGATCCGAGACAAAATGATCAGCGAAGAGATCTGAACCATCACAT 900
DB 790 ACCGTCTCTCAGAGATCCGAGACAAAATGATCAGCGAAGAGATCTGAACCATCACAT 849
QY 901 CACCATTAAGTGAAGCTT 918
DB 850 CACCATTAAGTGAAGCTT 867

```

## RESULT 4

US-09-782-397-18/c  
 ; Sequence 18, Application US/09782397  
 ; Publication No. US20030021779A1

## GENERAL INFORMATION:

APPLICANT: Dan, Michael D.  
 Mailli, Pradip K.  
 Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE

FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster LLP

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/782,397

FILING DATE: 13-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/862,124

FILING DATE: 1997-05-22

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 867 base pairs

TYPE: nucleic acid

STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
 US-09-782-397-18

Query Match 86.9%; Score 798; DB 11; Length 867;  
 Best Local Similarity 93.9%; Pred. No. 3.2e-233;  
 Matches 862; Conservative 0; Mismatches 5; Indels 51; Gaps 1;

```

QY 1 GAATTCATGAAAAAAACCGCTATCGCATCGCATGTCATCGCTGGTGGTTCCTACCGTT 60
DB 867 GAATTCATGAAAAAAACCGCTATCGCATCGCATGTCATCGCTGGTGGTTCCTACCGTT 808
QY 61 GCCGAGGCGCATATTTGTTTGAAGCATCTCCAGGCACTCTGTTTGTCTCCAGGGAA 120
DB 807 GCCGAGGCGCATATTTGTTTGAAGCATCTCCAGGCACTCTGTTTGTCTCCAGGGAA 748
QY 121 AGAGCCACCTCTCTCTGAGAGGCGCAGTCAGAGTGTAGTACAGCTACTAGCTGGTAC 180
DB 747 AGAGCCACCTCTCTCTGAGAGGCGCAGTCAGAGTGTAGTACAGCTACTAGCTGGTAC 688
QY 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGTCATCCACAGGCGCACT 240
DB 687 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGTCATCCACAGGCGCACT 628
QY 241 GGCATGCCAGACAGGTTCACTGAGTGGGTCCGGGACAGACTTCACTCAACATCACT 300
DB 627 GGCATGCCAGACAGGTTCACTGAGTGGGTCCGGGACAGACTTCACTCAACATCACT 568
QY 301 AGACTGAGGCTGAAATTTTGCAGTGTATTAATGTCAAGATGATGATGATGATGATGAT 360
DB 567 AGACTGAGGCTGAAATTTTGCAGTGTATTAATGTCAAGATGATGATGATGATGATGAT 508
QY 361 ACACTCAGATCACTTTGCGGAGGAGCCAAAGTGAATCAACGAACTGTGGCTGCA 420
DB 507 ACACTCAGATCACTTTGCGGAGGAGCCAAAGTGAATCAACGAACTGTGGCTGCA 448
QY 421 CCAATGCTCTGCGGCGGTGCGGCTTCCGAGAGTGTGATCAAGTGGAGTGGCTCCGAG 480
DB 447 TC-----CGAGAC 439
QY 481 GTGCACTGTGAGTCTGCGGAGGCGGTGTCACGCTGGAGAGTCCCTGAGACTCTCC 540
DB 438 GTGCACTGTGAGTCTGCGGAGGCGGTGTCACGCTGGAGAGTCCCTGAGACTCTCC 379
QY 541 TGTGCAAGCTCTGAGATTCCTCTTCAAGAGCTTTGCTATGCACTGGTCCGCAAGCTCTA 600
DB 378 TGTGCAAGCTCTGAGATTCCTCTTCAAGAGCTTTGCTATGCACTGGTCCGCAAGCTCTA 319
QY 601 GGCAGAGGGGCTGAGTGGGTGGGTCAGTTATATCATATGAGAGCACTAAATCTACGCA 660
DB 318 GGCAGAGGGGCTGAGTGGGTGGGTCAGTTATATCATATGAGAGCACTAAATCTACGCA 259
QY 661 GACTCCGTGAGAGGGCCGATTCACATCTCCAGAGACACTTCCAGAGACAGGCTGTATCTA 720
DB 258 GACTCCGTGAGAGGGCCGATTCACATCTCCAGAGACACTTCCAGAGACAGGCTGTATCTA 199
QY 721 AAATGAGACAGGCTGAGAACTGAGACACGCGTGTATTACTGTGCGAGATGAGAC 780
DB 198 AAATGAGACAGGCTGAGAACTGAGACACGCGTGTATTACTGTGCGAGATGAGAC 139
QY 781 CTGTTGGGTGACTATGACCACTACTACGTTTGAAGCTGTGGGCAAGGACACGCTC 840
DB 138 CTGTTGGGTGACTATGACCACTACTACGTTTGAAGCTGTGGGCAAGGACACGCTC 79
QY 841 ACCGTCTCTCAGAGATCCGAGACAAAATGATCAGCGAAGAGATCTGAACCATCACAT 900
DB 78 ACCGTCTCTCAGAGATCCGAGACAAAATGATCAGCGAAGAGATCTGAACCATCACAT 19
QY 901 CACCATTAAGTGAAGCTT 918
DB 18 CACCATTAAGTGAAGCTT 1

```

RESULT 5  
US-09-782-397-6/c  
; Sequence 6, Application US/09782397  
; Publication No. US20030021779A1  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
Maiti, Pradip K.  
Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 450 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-782-397-6

Query Match 39.3%; Score 361; DB 11; Length 450;  
Best Local Similarity 100.0%; Pred. No. 66-100;  
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 GATATTGTTGACGAGTCTCCAGGACCCCTGTTTGTCTCCAGGGGAAAGAGCCACC 129  
DB 378 GATATTGTTGACGAGTCTCCAGGACCCCTGTTTGTCTCCAGGGGAAAGAGCCACC 319  
QY 130 CTCTCTGAGGGCCAGTGAAGTGTAGTGAAGAGCTACTTACCTGSTRACCGAGAAA 189  
DB 318 CTCTCTGAGGGCCAGTGAAGTGTAGTGAAGAGCTACTTACCTGSTRACCGAGAAA 259  
QY 190 CCTGCGCAGGCTCCAGGCTCCTCATCTATGAGTATCCAGGAGCACTGCGATGCCA 249  
DB 258 CTGCGCAGGCTCCAGGCTCCTCATCTATGAGTATCCAGGAGCACTGCGATGCCA 199  
QY 250 GACAGGTTAGTGGCAGTGGGTCCGGGACAGACTTCACTTCACATCAGTAGACTGGAG 309  
DB 198 GACAGGTTAGTGGCAGTGGGTCCGGGACAGACTTCACTTCACATCAGTAGACTGGAG 139  
QY 310 CCTGAAGATTTTGCAGTGTATTACTGTCAAGCAATATGTAAGCTACCTCAGACACTCAG 369  
DB 138 CCTGAAGATTTTGCAGTGTATTACTGTCAAGCAATATGTAAGCTACCTCAGACACTCAG 79

QY 370 ATCATTTTGGCGGAGGAGCAAGTGAATCAACGAAGTGTGCTGCACCATCTGTC 429  
DB 78 ATCATTTTGGCGGAGGAGCAAGTGAATCAACGAAGTGTGCTGCACCATCTGTC 19  
QY 430 T 430  
DB 18 T 18

RESULT 6  
US-09-782-397-4  
; Sequence 4, Application US/09782397  
; Publication No. US20030021779A1  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
Maiti, Pradip K.  
Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 450 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..450  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-782-397-4

Query Match 39.2%; Score 359.4; DB 11; Length 450;  
Best Local Similarity 99.7%; Pred. No. 1.9e-99;  
Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 70 GATATTGTTGACGAGTCTCCAGGACCCCTGTTTGTCTCCAGGGGAAAGAGCCACC 129  
DB 72 GATATTGTTGACGAGTCTCCAGGACCCCTGTTTGTCTCCAGGGGAAAGAGCCACC 132  
QY 130 CTCTCTGAGGGCCAGTGAAGTGTAGTGAAGAGCTACTTACCTGSTRACCGAGAAA 189  
DB 133 CTCTCTGAGGGCCAGTGAAGTGTAGTGAAGAGCTACTTACCTGSTRACCGAGAAA 192

QY 190 CCTGGCCAGGCTCCAGGCTCTCATCTATGATGATCCAGGAGCCACTGGCATGCCA 249  
Db 193 CCTGGCCAGGCTCCAGGCTCTCATCTATGATGATCCAGGAGCCACTGGCATGCCA 252  
QY 250 GACAGGTTCACTGAGGAGTGGTCCGGGACAGACTTCACTCTTACATCATGAGTGGAG 309  
Db 253 GACAGGTTCACTGAGGAGTGGTCCGGGACAGACTTCACTCTTACATCATGAGTGGAG 312  
QY 310 CCTGAAGATTGTCAGTGTATTAATGTCAGAGTATGAGTCACTCACTCAAGACCTGAG 369  
Db 313 CCTGAAGATTGTCAGTGTATTAATGTCAGAGTATGAGTCACTCACTCAAGACCTGAG 372  
QY 370 ATCACTTTGGCGGAGGAGCCAGGTGAGATCAACGAACTGTGGCTGACCATCTGTC 429  
Db 373 ATCACTTTGGCGGAGGAGCCAGGTGAGATCAACGAACTGTGGCTGACCATCTGTC 432  
QY 430 T 430  
Db 433 T 433

## RESULT 7

US-09-782-397-1  
Sequence 1, Application US/09782397  
Publication No. US20030021779A1  
GENERAL INFORMATION:

APPLICANT: Dan, Michael D.  
Maiti, Pradip K.

Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA

COUNTRY: USA  
ZIP: 94304-1018

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 543 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..543

SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-782-397-1

Query Match 35.3%; Score 324.4; DB 11; Length 543;  
Best Local Similarity 89.3%; Pred. No. 9,5e-89;  
Matches 349; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 440 GCGGTTCCGAGGTGTGATCAGTGAAGTGGCTCCAGGTGACCTGAGTGGAGTCTG 499  
Db 152 GGGTTTCCCTGTTGCTCTTTTAAGAGTATCCAGTGTGAGGTGAGTGGAGTCTG 211  
QY 500 GGGAGGCGGAGTCCAGGCTGGAGGTCCCTGAGCTTCCTGAGGCTCGATATCC 559  
Db 212 GGGAGGCGGAGTCCAGGCTGGAGGTCCCTGAGCTTCCTGAGGCTCGATATCC 271  
QY 560 CTTCAAGACTTTGCTATGACATGAGTCCGAGGCTTAGCAAGGAGGCTGAGTGG 619  
Db 272 CTTCAAGACTTTGCTATGACATGAGTCCGAGGCTTAGCAAGGAGGCTGAGTGG 331  
QY 620 TGGCAGTTATATATATGATGAGAACATTAATCTACGACAGCTCCGTGAAGGCGCAT 679  
Db 332 TGGCAGTTATATATATGATGAGAACATTAATCTACGACAGCTCCGTGAAGGCGCAT 391  
QY 680 TCACCATCTCCAGAGACATTCAGAGAACAGCGGTATCTAAATAAGAACAGCTGAGAA 739  
Db 392 TCACCATCTCCAGAGACATTCAGAGAACAGCGGTATCTAAATAAGAACAGCTGAGAA 451  
QY 740 CTGAGGACAGCGCTGTCTATTAATCTGTGCGAGAGATCAGAGCTGTGGTGAATGACC 799  
Db 452 CTGAGGACAGCGCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 511  
QY 800 ACTACTAAGGTTGAGAGCTGTGGGGAAGG 830  
Db 512 ACTACTAAGGTTGAGAGCTGTGGGGAAGG 542

## RESULT 8

US-09-782-397-3/C

Sequence 3, Application US/09782397  
Publication No. US20030021779A1  
GENERAL INFORMATION:

APPLICANT: Dan, Michael D.  
Maiti, Pradip K.

Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA

COUNTRY: USA  
ZIP: 94304-1018

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792

TELEX: 706141  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 543 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-782-397-3

Query Match 35.3%; Score 324.4; DB 11; Length 543;  
Best Local Similarity 89.3%; Pred. No. 9.5e-89; Indels 0; Gaps 0;  
Matches 349; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 440 GCGGTTCCGAGGTGCTGATCAGTGTGAGTGTCTCCAGTGTGAGTGTGAGTGTG 499  
DB 392 GGGTTTCTCGTGTGCTTTTAAGAGTATCCAGTGTGAGTGTGAGTGTGAGTGTG 333  
QY 500 GGGAGGCGGTGTGCTGAGCTGGAGGTCTCTGAGACTCTCTGTGAGCTCTGAGTTC 559  
DB 332 GGGAGGCGGTGTGCTGAGCTGGAGGTCTCTGAGACTCTCTGTGAGCTCTGAGTTC 273  
QY 560 CCTTGAGAGCTTGTGATGACATGAGGTCCGAGGCTTGAAGGAGGAGGAGTGG 619  
DB 272 CCTTGAGAGCTTGTGATGACATGAGGTCCGAGGCTTGAAGGAGGAGTGG 213  
QY 620 TGGCAGTATATCATATGATGAGACATTAATACGACATCCGTGAGAGGCGAT 679  
DB 212 TGGCAGTATATCATATGATGAGACATTAATACGACATCCGTGAGAGGCGAT 153  
QY 680 TCACCATCTCCAGAGACACTTCCAGAGACAGGTGTATCTAAATGAAACAGCTGAGAA 739  
DB 152 TCACCATCTCCAGAGACACTTCCAGAGACAGGTGTATCTAAATGAAACAGCTGAGAA 93  
QY 740 CTGAGAGACAGGCTGTCTATTACTGTGCGAGAGATGAGAGCTGTGGGTATGATGAC 799  
DB 92 CTGAGAGACAGGCTGTCTATTACTGTGCGAGAGATGAGAGCTGTGGGTATGATGAC 33  
QY 800 ACTACTACGATTGAGAGCTGTGGGAGAG 830  
DB 32 ACTACTACGATTGAGAGCTGTGGGAGAGG 2

RESULT 9  
US-10-153-382-16  
Sequence 16, Application US/10153382  
Publication No. US20030086930A1  
GENERAL INFORMATION:  
APPLICANT: Pfizer Products Inc.  
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES  
FILE REFERENCE: PC23019A  
CURRENT APPLICATION NUMBER: US/10/153,382  
PRIOR FILING DATE: 2002-05-22  
PRIOR APPLICATION NUMBER: 60/293042  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 16  
LENGTH: 1413  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-153-382-16

Query Match 34.8%; Score 319.8; DB 14; Length 1413;  
Best Local Similarity 85.2%; Pred. No. 3.3e-87; Indels 0; Gaps 0;  
Matches 357; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 440 GCGGTTCCGAGGTGCTGATCAGTGTGAGTGTCTCCAGTGTGAGTGTGAGTGTG 499  
DB 20 GGGTTTCTCGTGTGCTTTTAAGAGTATCCAGTGTGAGTGTGAGTGTGAGTGTG 79  
QY 500 GGGAGGCGGTGTGCTGAGCTGGAGGTCTCTGAGACTCTCTGTGAGCTCTGAGTTC 559

DB 80 GGGAGGCGGTGTGCTGAGCTGGAGGTCCCTGAGACTCTCTGTGAGGCTGTGATTC 139  
QY 560 CCTTGAGAGCTTGTGATGACATGAGGTCCGAGGCTTGAAGGAGGAGTGG 619  
DB 140 CCTTGAGAGCTTGTGATGACATGAGGTCCGAGGCTTGAAGGAGGAGTGG 199  
QY 620 TGGCAGTATATCATATGATGAGACATTAATACGACATCCGTGAGAGGCGAT 679  
DB 200 TGGCAGTATATGATGATGAGAAATTAATATGATGAGACTCCGTGAGAGGCGAT 259  
QY 680 TCACCATCTCCAGAGACACTTCCAGAGACAGGTGTATCTAAATGAAACAGCTGAGAA 739  
DB 260 TCACCATCTCCAGAGACACTTCCAGAGACAGGTGTATCTGAAATGAAACAGCTGAGAG 319  
QY 740 CTGAGAGACAGGCTGTCTATTACTGTGCGAGAGATGAGAGCTGTGGGTATGATGAC 799  
DB 320 CTGAGAGACAGGCTGTCTATTACTGTGCGAGAGATGAGAGGAGCTTATCTACT 379  
QY 800 ACTACTACGATTGAGAGCTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 858  
DB 380 ACTACTACGATTGAGAGCTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 438

RESULT 10  
US-09-453-234-49  
Sequence 49, Application US/09453234  
Publication No. US20030091995A1  
GENERAL INFORMATION:  
APPLICANT: Buehler, Joe  
APPLICANT: Valakis, Gunars  
APPLICANT: Gray, Jeff  
APPLICANT: Lombard, Nils  
APPLICANT: Biosite Diagnostics, Inc.  
APPLICANT: Genpharm International  
TITLE OF INVENTION: Human Antibodies  
FILE REFERENCE: 020015-000110US  
CURRENT APPLICATION NUMBER: US/09/453,234  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: US 60/157,415  
NUMBER OF SEQ ID NOS: 112  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 49  
LENGTH: 678  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: M1-23L  
NAME/KEY: CDS  
LOCATION: (1)..(678)  
US-09-453-234-49

Query Match 33.8%; Score 310.6; DB 11; Length 678;  
Best Local Similarity 93.6%; Pred. No. 1.7e-84;  
Matches 338; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

QY 70 GATATTGTTGACGAGTCTCCAGGACCTGTCTTTGTCTCCAGGGAGAGAGGACAC 129  
DB 1 GAAATTTGTTGACGAGTCTCCAGGACCTGTCTTTGTCTCCAGGGAGAGAGGACAC 60  
QY 130 CTCTCTGAGAGGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTG 189  
DB 61 CTCTCTGAGAGGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTG 120  
QY 190 CTCTCTGAGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATG 249  
DB 121 CTCTCTGAGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATG 180  
QY 250 GACAGTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 309  
DB 181 GACAGTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 240  
QY 310 CCTGAGATTTTGTGAGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 369

```
Db 241 CCTGAAGATTGTCAGTGTATTACTGTCTGACGAGTATGGTAGCT-----CACCTCG 291
Qy 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAACCAACTGTGGCTGCACCATCTGTC 429
Db 292 TACACTTTGGCGGAGGAGCAAGGTGAGATCAACCAACTGTGGCTGCACCATCTGTC 351
Qy 430 T 430
Db 352 T 352
```

RESULT 11  
US-09-453-234-85

```
; Sequence 85, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(678)
; OTHER INFORMATION: M2-33L
US-09-453-234-85
```

Query Match 33.8%; Score 310.6; DB 11; Length 678;  
Best Local Similarity 93.6%; Pred. No. 1.7e-84;  
Matches 338; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

```
Qy 70 GATATTGTTGAGCGAGTCTCCAGGCACTCTGTTGTTCTCCAGGGGAAAGGCCACC 129
Db 1 GAAATGTGTGAGCGAGTCTCCAGGCACTCTGTTGTTCTCCAGGGGAAAGGCCACC 60
Qy 130 CTCTCCTGCGAGGGCCAGTCAAGTGTAGTGAAGCTAAGCTGCTGATCAGACAGAAA 189
Db 61 CTCTCCTGCGAGGGCCAGTCAAGTGTAGTGAAGCTAAGCTGCTGATCAGACAGAAA 120
Qy 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGTTGATCACCAGGCGCATGGGATGCCA 249
Db 121 CTTGGCCAGGCTCCAGGCTCTCATCTATGTTGATCACCAGGCGCATGGGATGCCA 180
Qy 250 GACAGGTTCAAGTGGAGTGGGTCCGGGACAGACTTCACTTCAACATGATGAAGTGGAG 309
Db 181 GACAGGTTCAAGTGGAGTGGGTCTGGGACAGACTTCACTTCAACATGAGAGCTGGAG 240
Qy 310 CCTGAAGATTTTGGAGTGTATTACTGTGAGCAGTATGGTAGCTCAACCTCAGACACTCAG 369
Db 241 CCTGAAGATTTTGGAGTGTATTACTGTGAGCAGTATGGTAGCT-----CACCTCG 291
Qy 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAACCAACTGTGGCTGCACCATCTGTC 429
Db 292 TACACTTTGGCGGAGGAGCAAGGTGAGATCAACCAACTGTGGCTGCACCATCTGTC 351
Qy 430 T 430
Db 352 T 352
```

RESULT 12  
US-09-453-234-37

```
; Sequence 37, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(678)
US-09-453-234-37
```

Query Match 33.3%; Score 305.8; DB 11; Length 678;  
Best Local Similarity 92.8%; Pred. No. 4.9e-83;  
Matches 335; Conservative 0; Mismatches 17; Indels 9; Gaps 1;

```
Qy 70 GATATTGTTGAGCGAGTCTCCAGGCACTCTGTTGTTCTCCAGGGGAAAGGCCACC 129
Db 1 GAAATGTGTGAGCGAGTCTCCAGGCACTCTGTTGTTCTCCAGGGGAAAGGCCACC 60
Qy 130 CTCTCCTGCGAGGGCCAGTCAAGTGTAGTGAAGCTAAGCTGCTGATCAGACAGAAA 189
Db 61 CTCTCCTGCGAGGGCCAGTCAAGTGTAGTGAAGCTAAGCTGCTGATCAGACAGAAA 120
Qy 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGTTGATCACCAGGCGCATGGGATGCCA 249
Db 121 CTTGGCCAGGCTCCAGGCTCTCATCTATGTTGATCACCAGGCGCATGGGATGCCA 180
Qy 250 GACAGGTTCAAGTGGAGTGGGTCCGGGACAGACTTCACTTCAACATGATGAAGTGGAG 309
Db 181 GACAGGTTCAAGTGGAGTGGGTCTGGGACAGACTTCACTTCAACATGAGAGCTGGAG 240
Qy 310 CCTGAAGATTTTGGAGTGTATTACTGTGAGCAGTATGGTAGCTCAACCTCAGACACTCAG 369
Db 241 CCTGAAGATTTTGGAGTGTATTACTGTGAGCAGTATGGTAGCT-----CACCTCA 291
Qy 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAACCAACTGTGGCTGCACCATCTGTC 429
Db 292 TTAACCTTTGGCGGAGGAGCAAGGTGAGATCAACCAACTGTGGCTGCACCATCTGTC 351
Qy 430 T 430
Db 352 T 352
```

RESULT 13  
US-09-453-234-41

```
; Sequence 41, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
```

```

1  APPLICANT: GenPharm International
2  TITLE OF INVENTION: Human Antibodies
3  FILE REFERENCE: 020015-000110US
4  CURRENT APPLICATION NUMBER: US/09/453,233
5  CURRENT FILING DATE: 1999-12-01
6  PRIOR APPLICATION NUMBER: US 60/157,415
7  PRIOR FILING DATE: 1999-10-02
8  NUMBER OF SEQ ID NOS: 112
9  SOFTWARE: Patencin Ver. 2.1
10
11  SEQ ID NO 41
12
13  LENGTH: 678
14
15  TYPE: DNA
16
17  ORGANISM: Homo sapiens
18
19  FEATURE:
20  NAME/KEY: CDS
21  LOCATION: (1)..(678)
22
23  OTHER INFORMATION: M1-5L
24
25  US-09-453-234-41

```

Query Match	33.3%	Score 305.8	DB 11	Length 678
Best Local Similarity	92.8%	Pred. No. 4.9e-83		
Matches 335, Conservative	0	Mismatches 17	Indels 9	Gaps 1

Oy	70	GATATGTTGTAACGCACTCCAGGACCCCTGCTTTGTCACAGGGAAAGACACC	123
Db	1	GAAATAGTATACGACAGTCTCCAGGACCCCTGCTTTGTCACAGGGAAAGACACC	60
Oy	130	CTCTCTCGAGGGCCAGTCAGAGTGTATTAGCAGCTACTTAACCTGGTACAGCAGAAA	183
Db	61	CTCTCTCGAGGGCCAGTCAGAGTGTATTAGCAGCAGCTACTTAACCTGGTACAGCAGAAA	120
Oy	150	CCTGGCCAGGCTTCCAGGCTCCTCATCTATGTGTCATCCACAGGGCCACTGGCATGCCA	249
Db	121	CCTGGCCAGGCTTCCAGGCTCCTCATCTATGTGTCATCCACAGGGCCACTGGCATGCCA	180
Oy	250	GACAGGTCAGTGGCAGTGGGTCCGGGACAGATTCACTCTCAACATCACTAGACTGGAG	305
Db	181	GACAGGTCAGTGGCAGTGGGTCTGGGACAGACTTCACTTCAACATCAACAGACTGGAG	240
Oy	310	CCTGAAGATTTTGCAGTGTATTACTGTGCAGCAGTATGTTGCTCACTCAGACACCTCAG	363
Db	241	CCTGAAGATTTTGCAGTGTATTACTGTGCAGCAGTATGTTGCT-----CACTATA	291
Oy	370	ATCACTTTTCGCGGAGGGACCAAGGTGAGATCAAAAGAACTGGCTGCACCATCTGTC	429
Db	292	TTCACTTTTCGCGCTGGGACCAAAAGTGATATCAAAAGAACTGGCTGCACCATCTGTC	351
Oy	430	T 430	
Db	352	T 352	

```

RESULT 14
US-09-453-234-71
Sequence 71, Application US/09453234
Publication No. US20030091995A1
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valitov, Gunare
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, Nile
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/457,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 71
LENGTH: 678

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(678)
; OTHER INFORMATION: M2-11L
US-09-453-234-71

```

Query Match	33.3%	Score 305.8	DB 11	Length 678
Best Local Similarity	92.8%	Pred. No. 4.9e-83		
Matches 335, Conservative	0	Mismatches 17	Indels 9	Gaps 1

Qy	70	GAATATGTGTTGACGCAAGTCTCAGGACACCTGTCTTTGTCTCCAGGGGAAAGACACC	125
Db	1	GAATATGTATGACGCAAGTCTCAGGACACCTGTCTTTGTCTCCAGGGGAAAGACACC	60
Qy	130	CTCTCTGCAAGGCGCAGTCAGAGTGTAGTAGCAGCTTACCTGTGTACAGCAGAA	185
Db	61	CTCTCTGCAAGGCGCAGTCAGAGTGTAGTAGCAGCAGCTTACCTGTGTACAGCAGAA	125
Qy	190	CTGTGGCAGGCTTCCAGGCTCTCTCATCTATGTGTGATCCACAGGGCCACTGTGCATGCCA	245
Db	121	CTGTGGCAGGCTTCCAGGCTCTCTCATCTATGTGTGATCCACAGGGCCACTGTGCATGCCA	180
Qy	250	GACAGGTCAGTGGGAGTGGGATCCGGGACAGACTTCATCCATCAGTACAGTGGAG	305
Db	181	GACAGGTCAGTGGGAGTGGGATCTGGGACAGACTTCATCCATCAGTACAGTGGAG	240
Qy	310	CTGGAAGATTTTGCAGGTGTATTACTGTACAGCATATGTACTCACTCAGACACCTCAG	365
Db	241	CTGGAAGATTTTGCAGGTGTATTACTGTACAGCATATGTACTCT-----CACTCTCA	291
Qy	370	ATGACTTTTGGGGGAGGAGGACCAAGGTGAGATCAAAAGAACTGTGGCTGCACATCTGTGC	425
Db	292	TTTACTTTTGGGCGCTGGGACCAAAAGTGAATCAAAACGAACGTGTGGCTGCACATCTGTGC	351
Qy	430	T	430
Db	352	T	352

```

RESULT 15
US-10-041-860-59
Sequence 59, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvatan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX, 051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 379
TYPE: DNA
ORGANISM: homo sapiens
US-10-041-860-59

```

```

Query Match:      33.1%; Score 303.8; DB 12; Length 379;
Best Local Similarity 89.4%; Pred. No. 1.6e-82;
Matches 339; Conservative 0; Mismatches 37; Indels 3; Gaps 1
QY      478 CAGGCCACTGCTGGAGTCTGGGGAGAGCCTGATCAGCCTGGGAGTCCCTGAGCTC 537
|||||

```

```
Db      1 CAGGTGCACTGTGGAGTCCGGGGAGGCGGTGTCAGCCTGGGAAATCCCTGAGACTC 60
QY      538 TCCTGTGAGGCTCTGGAATCCCTTCAGAACTTTGCTATGCACTGGTCCGCCAGGCT 597
Db      61 TCCTGTGAGGCTCTGGAATCCCTTCAGAACTTTGCTATGCACTGGTCCGCCAGGCT 120
QY      598 CTAGGCAGGGGCTGGAGTGGGTGGCAGTTATATGATGGAAGCACTAAATACTAC 657
Db      121 CCAGGCAGGGGCTGGAGTGGGTGGCAGTTATATGATGGAAGCACTAAATACTAT 180
QY      658 GCAGACTCCGTGAAGGGCCGATTCAACATCTCCAGAGACACTCCAGAAACACGGTGAT 717
Db      181 GCAGACTCCGTGAAGGGCCGATTCAACATCTCCAGAGACACTCCAGAAACACGGTGAT 240
QY      718 CTAAATATGAACAGCCTGAGAACTGAGGACACGGCTGTCTATTACTGTGCGAGAGATCAG 777
Db      241 CTGCAATATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCAA 300
QY      778 AG---CCTGTGGGTGACTATGACCACTACTACGTTTGGACGTCTGGGGCAAGGAC 834
Db      301 GGATACAGATATGCTGTACTACTACGACTACGGTATGACGTCCTGGGGCCAAAGGAC 360
QY      835 ACGGTACCGTCTCTCTCAG 853
Db      361 ACGGTACCGTCTCTCTCAG 379
```

Search completed: September 17, 2003, 05:31:54  
Job time : 876 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 02:57:14 ; Search time 1933 Seconds  
(without alignments)  
11542.426 Million cell updates/sec

Title: US-08-657-449-13

Perfect score: 918  
Sequence: 1 GATTTCATGAAAAAACCCG.....ATCACCATTAGTGAAGCTT 918

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_escba:\*  
2: em\_escba:\*  
3: em\_escba:\*  
4: em\_escba:\*  
5: em\_escba:\*  
6: em\_escba:\*  
7: em\_escba:\*  
8: em\_escba:\*  
9: gb\_esc1:\*  
10: gb\_esc2:\*  
11: gb\_esc3:\*  
12: gb\_esc4:\*  
13: gb\_esc4:\*  
14: gb\_esc5:\*  
15: em\_escfun:\*  
16: em\_escfun:\*  
17: em\_escfun:\*  
18: em\_escfun:\*  
19: em\_escfun:\*  
20: em\_escfun:\*  
21: em\_escfun:\*  
22: em\_escfun:\*  
23: em\_escfun:\*  
24: em\_escfun:\*  
25: em\_escfun:\*  
26: em\_escfun:\*  
27: em\_escfun:\*  
28: gb\_esc1:\*  
29: gb\_esc2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	317.6	34.6	584	10	BF664453	BF664453 602146204
2	314.8	34.3	516	9	AW401728	AW401728 UI-HF-BKO
3	313.4	34.1	536	9	AW402624	AW402624 UI-HF-BKO
4	311	33.9	881	13	BQ709375	BQ709375 AGENCOURT

5	310.6	33.8	979	13	BQ709399	BQ709399 AGENCOURT
6	309	33.7	424	10	BF874079	BF874079 IL3-ET011
7	308.6	33.6	566	9	AW405972	AW405972 UI-HF-BLO
8	308	33.6	745	12	B1759245	B1759245 603042678
9	307.8	33.5	433	9	AV647117	AV647117 AV647117
10	307.8	33.5	440	9	AV647111	AV647111 AV647111
11	307.8	33.5	504	9	AW405787	AW405787 UI-HF-BLO
12	307.8	33.5	734	10	BG686748	BG686748 602650717
13	307.8	33.5	793	9	AV646708	AV646708 AV646708
14	307.8	33.5	926	13	BQ706614	BQ706614 AGENCOURT
15	307.8	33.5	998	13	BQ709245	BQ709245 AGENCOURT
16	307.2	33.4	801	13	BK399298	BK399298 BK399298
17	306.2	33.4	518	9	AW406576	AW406576 UI-HF-BLO
18	306.2	33.4	862	10	BG758749	BG758749 602713108
19	306.2	33.4	1014	12	BM918339	BM918339 AGENCOURT
20	306	33.3	456	9	AW406451	AW406451 UI-HF-BLO
21	305.8	33.3	472	9	AW405697	AW405697 UI-HF-BLO
22	305.8	33.3	603	9	AW404910	AW404910 UI-HF-BLO
23	304.6	33.2	933	13	BQ711272	BQ711272 AGENCOURT
24	304.2	33.1	526	13	BQ331002	BQ331002 QV3-ET019
25	303.8	33.1	1069	12	BM919414	BM919414 AGENCOURT
26	303.4	33.1	1153	10	BF663521	BF663521 602144686
27	303	33.0	441	10	BF914735	BF914735 IL3-UT011
28	303	33.0	441	10	BF914740	BF914740 IL3-UT011
29	303	33.0	488	12	BM830796	BM830796 K-EST0104
30	303	33.0	504	10	BF917294	BF917294 IL3-UT011
31	303	33.0	544	9	AW405216	AW405216 UI-HF-BLO
32	303	33.0	644	9	AW405817	AW405817 UI-HF-BLO
33	303	33.0	859	13	BK368110	BK368110 BK368110
34	303	33.0	923	13	BQ711051	BQ711051 AGENCOURT
35	303	33.0	974	13	BQ707037	BQ707037 AGENCOURT
36	302.6	33.0	489	9	AW406488	AW406488 UI-HF-BLO
37	302.4	32.9	1201	13	BK357917	BK357917 BK357917
38	301.8	32.9	976	12	BM914525	BM914525 AGENCOURT
39	301.4	32.8	978	13	BQ707988	BQ707988 AGENCOURT
40	301	32.8	786	14	CB956522	CB956522 AGENCOURT
41	301	32.8	917	13	BQ711815	BQ711815 AGENCOURT
42	300.6	32.7	718	14	CB957976	CB957976 AGENCOURT
43	299.8	32.7	707	10	BG685522	BG685522 602637389
44	299.8	32.7	786	14	CB957311	CB957311 AGENCOURT
45	299.8	32.7	840	10	BG685798	BG685798 602637907

## ALIGNMENTS

RESULT 1  
BF664453  
LOCUS 602146204F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4309680 5',  
DEFINITION mRNA sequence.  
ACCESSION BF664453.1 GI:11938258  
VERSION BF664453.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution/ILNL at:  
found through the I.M.A.G.E. Consortium/ILNL at:  
http://image.llnl.gov  
Plate: L1CML183 row: h column: 01  
High quality sequence stop: 584.

## FEATURES

Location/Qualifiers  
1. 584

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4309680"  
/tissue\_type="Primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_48"  
/note="Organ: B-cells; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

## BASE COUNT

139 a 168 c 153 g 124 t

## ORIGIN

Query Match 34.6%; Score 317.6; DB 10; Length 584;  
Best Local Similarity 87.3%; Pred. No. 2.7e-71;  
Matches 363; Conservative 0; Mismatches 44; Indels 9; Gaps 1;

15 AACGGTATGCGCATGCGAGTTCAGTGGCTGTTGGCTACCGTGGCAGGCCATAT 74  
17 AAACCCAGGCGAGCTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 76  
75 TGTGTGAGCGAGTCTTCAGGACCCCTGTTTGTCTTCAGGGGAAAGCCATCTCT 134  
77 TGTGTGAGCGAGTCTTCAGGACCCCTGTTTGTCTTCAGGGGAAAGCCATCTCT 136  
135 CTGCAAGGCGCAGTACAGTGTATGATGAGTCTTACCTGCTGTTACCAAGAAACCTGG 194  
137 CTGCAAGGCGCAGTACAGTGTATGATGAGTCTTACCTGCTGTTACCAAGAAACCTGG 196  
195 CCAAGGCTCCAGGCTCTCTATCTATGATGATTCACCAAGGCGCAGTGGCAATGCCAGAG 254  
197 CCAAGGCTCCAGGCTCTCTATCTATGATGATTCACCAAGGCGCAGTGGCAATGCCAGAG 256  
255 GTTCAGTGGCAGTGGGTCCGGGACAGACTTCACTCTCAACATCAGTACGAGCTGAG 314  
257 GTTCAGTGGCAGTGGGTCCGGGACAGACTTCACTCTCAACATCAGTACGAGCTGAG 316  
315 AGATTGTCAGTGTATCTCTGTCAGGATGATGATGATGATGATGATGATGATGATGAT 374  
317 AGATTGTCAGTGTATCTCTGTCAGGATGATGATGATGATGATGATGATGATGATGAT 367  
375 TTTCCGCGGAGGAGCAAGGATCAACGAACTGTGGCTGACCATCTGCT 430  
368 TTTCCGCGGAGGAGCAAGGATCAACGAACTGTGGCTGACCATCTGCT 423

RESULT 2  
AM401728 516 bp mRNA linear EST 16-FEB-2000  
LOCUS  
DEFINITION  
IMAGE:3053711 5', mRNA sequence.  
AM401728.1 GI:6920414  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
NIH-MGC http://mgc.ncl.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov  
Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Straud, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
cDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLT at:  
www-bio.lnlt.gov/bbrp/image/image.html  
Seq primer: M13 forward

## FEATURES

## source

Location/Qualifiers  
1. 516

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3053711"  
/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LT1)"  
/clone\_lib="NIH\_MGC\_36"  
/note="Vector: pT73-Pac; Site\_1: NotI; Site\_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Straud, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

## BASE COUNT

112 a 132 c 150 g 122 t

## ORIGIN

Query Match 34.3%; Score 314.8; DB 9; Length 516;  
Best Local Similarity 85.8%; Pred. No. 1.3e-70;  
Matches 362; Conservative 0; Mismatches 57; Indels 3; Gaps 1;

440 GCGGTTCCGGAGGTGGATGATCAGTGGAGTGGCTCCAGGCGCAGTGGTGAAGTTC 499  
93 GGGTTTCTCTGTTGCTCTTTAAGAGTGTCCAGTGTACAGTGGTGAAGTTC 152  
500 GGGAGGCGGTGTCCAGCTGGAGGCTCCCTGAGACTCTCTGTGAGCTCTGATTC 559  
153 GGGAGGCGGTGTCCAGCTGGAGGCTCCCTGAGACTCTCTGTGAGCTCTGATTC 212  
560 CTTTCAAGAGCTTGTCTATGACACTGGGTCCCGCAGCTCTAGGCAAGGGCTGAGTGG 619  
213 CTTTCAAGAGCTTGTCTATGACACTGGGTCCCGCAGCTCTAGGCAAGGGCTGAGTGG 272  
620 TGGCAATTAT 679  
273 TGGCAATTAT 332  
680 TCACCATCTCCAGAGACACTTCCAGAGACAGGCTGTATCTAAATATGACAGCTGAGAA 739  
333 TCACCATCTCCAGAGACACTTCCAGAGACAGGCTGTATCTGCAATATGACAGCTGAGAA 392  
740 CTGAGGACACGGCTGTCTTATCTGTGAGAGATGAGAGCC--TGTGGGTGACTATG 796  
393 CTGAGGACACGGCTGTCTTATCTGTGAGAGATGAGAGCCCTGTGCTTACGGTACTTCACTT 452  
797 ACCACTACTACGGTTTGAAGTCTGGGGGAAAGGAGCAAGGCTACCGTCTCTCAGAGAT 856  
453 ACTACTACTACGGTTATGAGAGTCTGGGGGAAAGGAGCAAGGCTACCGTCTCTCAGAGAT 512

## RESULT 3

AM402624 536 bp mRNA linear EST 16-FEB-2000  
LOCUS  
DEFINITION  
IMAGE:3053559 5', mRNA sequence.

AM402624  
VERSION  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
Homo sapiens

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 536)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabbs-r@mail.nih.gov  
 Eco RI site shown at the beginning of the sequence.  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 CDNA Library Preparation: M.B. Soares Lab  
 CDNA Library Arrayed by: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/dbp/image/image.html  
 Seq primer: M13 Forward

FEATURES  
 source  
 1..536  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:305359"  
 /issue\_type="lymph"  
 /cell\_line="germinal center B cells"  
 /lab\_host="DH10B (LTI)"  
 /clone\_1lb="NIH MGC 36"  
 /note="Vector: pTZ19-Pac; Site\_1: NotI; Site\_2: Eco RI;  
 Constructed from size fractionated cytoplasmic mRNA  
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis  
 M. Staudt, Ph.D. Library preparation by Maria de Fatima  
 Bonaldi, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 113 a 141 c 160 g 122 t

ORIGIN

Query Match 34.1%; Score 313.4; DB 9; Length 536;  
 Best Local Similarity 85.9%; Pred. No. 3.2e-70;  
 Matches 360; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

QY 440 GGGGTTCCGAGAGTGTGATCAGTGAAGTGGCTCCAGGTGACGCTGTGAGTCTG 499  
 Db 57 GGGTTTCTCGTGTCTTTAAAGAGTGTCCAGTGAAGTGAAGTGAAGTGAAGTCTG 116  
 QY 500 GGGGAGCGTGGTCCAGCTGGAGAGTCCCTGAGACTCTCTGTGAGCTCTGATTCC 559  
 Db 117 GGGGAGCGTGGTCCAGCTGGAGAGTCCCTGAGACTCTCTGTGAGCTCTGATTCA 176  
 QY 560 CCTTGAGAGCTTTGCTATGCACTGGGTCGCCAGGCTCTAGGCAAGGGCTGAGTGG 619  
 Db 177 CTTGAGTACTATGATGCACTGGGTCGCCAGGCTCTAGGCAAGGGCTGAGTGG 236  
 QY 620 TGGCAGTATATATGATGAGCACTAATATCTAGCAGACTCCGTGAAAGGCCGAT 679  
 Db 237 TGGCAGTATATATGATGAGCACTAATATCTAGCAGACTCCGTGAAAGGCCGAT 296  
 QY 680 TCACCATCTCCAGAGCACTCCAGAGACAGCGTGTATTAATAAATGAACAGCTGAGAA 739  
 Db 297 TCACCATCTCCAGAGCACTCCAGAGACAGCGTGTATGCAAAATGAACAGCTGAGAA 356  
 QY 740 CTGAGAGCAAGCGCTGTCTATTAATGCTGAGAGATCAGAGCTGTGGTGAATGACC 799  
 Db 357 CTGAGAGCAAGCGCTGTCTATTAATGCTGAGAGATGATGAC---TGTGTTTTGGGACT 413  
 QY 800 ACTACTACGCTTGGAGCGTGGGGCAAGGACCAAGCTGACCGTCTCTGAGCTCC 858  
 Db 414 ACTACTACGCTTGGAGCGTGGGGCAAGGACCAAGCTGACCGTCTCTGAGCTCC 472

RESULT 4  
 BQ709375 LOCUS BQ709375 881 bp mRNA linear EST 16-JUL-2002

DEFINITION AGENCOURT\_7977299 NIH\_MGC\_113 Homo sapiens CDNA clone IMAGE:6215729  
 5', mRNA sequence.  
 ACCESSION BQ709375  
 VERSION BQ709375.1 GI:21848274  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 881)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabbs-r@mail.nih.gov  
 Tissue Procurement: Dr. Mark Watson  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LCM2385 row: b column: 18  
 High quality sequence stop: 700.

FEATURES  
 source  
 1..881  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6215729"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_1lb="NIH MGC 113"  
 /note="Organ: spleen; Vector: pTZ19-Pac; Site\_1: XhoI; Site\_2:  
 EcoRI; CDNA made by oligo-dT priming. Directionally cloned  
 into EcoRI/XhoI sites using the following 5' adaptor:  
 GGCACGAG(G). Library constructed by Ling Hong in the  
 Laboratory of Gerald M. Rubin (University of California,  
 Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH MGC Library."

BASE COUNT 198 a 275 c 218 g 188 t 2 others

ORIGIN

Query Match 33.9%; Score 311; DB 13; Length 881;  
 Best Local Similarity 93.9%; Pred. No. 1.7e-69;  
 Matches 339; Conservative 0; Mismatches 10; Indels 12; Gaps 1;

QY 70 GATATGTTGTTGACGCACTCTCCAGGCAACCTGCTTTGCTCCAGGGGAAAGCCACC 129  
 Db 70 GAAATGTTGTTGACGCACTCTCCAGGCAACCTGCTTTGCTCCAGGGGAAAGCCACC 129  
 QY 130 CTTCTCCAGGCGCAGTCAAGTGTATGAGCACTACTTAACTGTTACAGAGAA 189  
 Db 130 CTTCTCCAGGCGCAGTCAAGTGTATGAGCACTACTTAACTGTTACAGAGAA 189  
 QY 190 CTTGACAGGCTCCAGGCTCTCATCTATGATGATGATGATGATGATGATGATGATGAT 249  
 Db 190 CTTGACAGGCTCCAGGCTCTCATCTATGATGATGATGATGATGATGATGATGATGAT 249  
 QY 250 GACAGTTCACTGAGTGGTCCGAGACAGCTTCACTTCAATCAGTCACTGAGTGG 309  
 Db 250 GACAGTTCACTGAGTGGTCCGAGACAGCTTCACTTCAATCAGTCACTGAGTGG 309  
 QY 260 GACAGTTCACTGAGTGGTCCGAGACAGCTTCACTTCAATCAGTCACTGAGTGG 309  
 Db 260 GACAGTTCACTGAGTGGTCCGAGACAGCTTCACTTCAATCAGTCACTGAGTGG 309  
 QY 310 CTTGAGATTTTGGAGTGTATTAATGCTGAGAGTATGATGATGATGATGATGATGATGAT 369  
 Db 310 CTTGAGATTTTGGAGTGTATTAATGCTGAGAGTATGATGATGATGATGATGATGATGAT 369  
 QY 370 ATCACTTTCGCGAGGAGCACAAGTGAAGATCAAGCAAGCTGTGAGTCACTGATCTGC 429  
 Db 358 GTCACTTTCGCGAGGAGCACAAGTGAAGATCAAGCAAGCTGTGAGTCACTGATCTGC 417

430 T 430

Db 418 T 418

RESULT 5  
BQ709399

LOCUS  
BQ709399

DEFINITION  
AGENCOURT 7972270 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6215847 5', mRNA sequence.

ACCESSION  
BQ709399

VERSION  
BQ709399.1

KEYWORDS  
GI:21848298

SOURCE  
Homo sapiens (human)

ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
1 (bases 1 to 979)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished

TITLE  
JOURNAL

COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
Plate: LICM2385 row: 9 column: 16  
High quality sequence stop: 401.  
Location/Qualifiers  
1..979

## FEATURES

source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6215847"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_11b="NIH MGC 113"  
/note="Organ: spleen; Vector: pORF7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC library"

BASE COUNT  
204 a 295 c 283 g 197 t

ORIGIN

Query Match 33.8%; Score 310.6; DB 13; Length 979;  
Best Local Similarity 93.6%; Pred. No. 2.2e-69;  
Matches 338; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

QY 70 GATTGTGTTGACGCGCTCCAGGACCCCTGTTGTTCTCCAGGGGAAAGCCACC 129

Db 80 GAATTTGTGTTGACGCGCTCCAGGACCCCTGTTGTTCTCCAGGGGAAAGCCACC 139

QY 130 CTCTCTGCGAGGGGCGAGTCAAGAGTTAGTACGCTTACCTGCTGCTCCAGGAA 189

Db 140 CTCTCTGCGAGGGGCGAGTCAAGAGTTAGTACGCTTACCTGCTGCTCCAGGAA 199

QY 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGCGCACTGGCATGCCA 249

Db 200 CTTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGCGCACTGGCATGCCA 259

QY 250 GACAGGTTGAGTGGCACTGGGTCCGGGACAGACTTCACTCAACCATCACTAGTGA 309

Db 260 GACAGGTTGAGTGGCACTGGGTCCGGGACAGACTTCACTCAACCATCACTAGTGA 319

QY 310 CCTGAAGATTTCAGTGTATTAATCTGTCAGAGATGATGATCACTCAAGACCTGAG 369

Db 320 CCTGAAGATTTCAGTGTATTAATCTGTCAGAGATGATGATCACTCAAGACCTGAG 370

QY 370 ATCATCTTGGCGGAGGAGCCAGAGTGGAGATCAACGAACTGTGCTGCACCATCTGC 429

Db 371 ATCATCTTGGCGGAGGAGCCAGAGTGGAGATCAACGAACTGTGCTGCACCATCTGC 430

QY 430 T 430

Db 431 T 431

RESULT 6  
BF874079

LOCUS  
BF874079

DEFINITION  
IL3-ET0115-071100-302-D08 ET0115 Homo sapiens cDNA, mRNA sequence.

ACCESSION  
BF874079

VERSION  
BF874079.1

KEYWORDS  
GI:12264209

SOURCE  
Homo sapiens (human)

ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
1 (bases 1 to 424)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Coستا, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.V.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
10737800

COMMENT  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL3&t2=IL3-ET0115-071100-302-D08&t3=2000-11-07&t4=1>)  
Seq. primer: puc 18 forward  
High quality sequence stop: 392.  
Location/Qualifiers  
1..424

## FEATURES

source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_11b="ET0115"  
/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT  
90 a 127 c 111 g 96 t

ORIGIN

Query Match 33.7%; Score 309; DB 10; Length 424;  
Best Local Similarity 93.4%; Pred. No. 3.9e-69;  
Matches 337; Conservative 0; Mismatches 15; Indels 9; Gaps 1;

QY 70 GATTGTGTTGACCGAGTCTCCAGGACCCCTGTTGTTCTCCAGGGGAAAGCCACC 129

Db 61 GAATTTGTGTTGACCGAGTCTCCAGGACCCCTGTTGTTCTCCAGGGGAAAGCCACC 120

QY 130 CTCTCTGCGAGGGGCGAGTCAAGAGTTAGTACGCTTACCTGCTGCTCCAGGAA 189

Db 121 CTCCTCGACGGCCAGTCAAGATTGACGACGACTTACCTTGCTGACGACGAGG 180  
 Qy 190 CCTGGCAGAGCTCCAGAGCTCTCATCTATGTCATCCACGAGGCCACTGGCATGCCA 249  
 Db 181 CCGGGCAGAGCTCCAGAGCTCTCATCTATGTCATCCACGAGGCCACTGGCATGCCA 240  
 Qy 250 GACAGGTTCAAGTGGCAGTGGGTCCGGACAGACTTCACTTCACCATCAGTAGACTGGAG 309  
 Db 241 GACAGGTTCAAGTGGCAGTGGGTCTGGGACAGACTTCACTTCACCATCAGTAGAG 300  
 Qy 310 CCGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGTCAGTCACTCAGACCTCGAG 369  
 Db 301 CCGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGTCAGTCACTCAGACCTCGAG 351  
 Qy 370 ATCACTTTGGCGGAGGACCAAGTGGAGATCAACGAACTGTGGCTGCACCATCTGTC 429  
 Db 352 CTCACCTTTGGCGGAGGACCAAGTGGAGATCAACGAACTGTGGCTGCACCATCTGTC 411  
 Qy 430 T 430  
 Db 412 T 412

RESULT 7  
 AM405972 566 bp mRNA linear EST 16-FEB-2000  
 LOCUS UI-HF-BL0-acv-a-01-0-UI.r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
 DEFINITION IMAGE:3060360 5', mRNA sequence.  
 ACCESSION AM405972  
 VERSION AM405972.1 GI:6925029  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
 JOURNAL 1 (bases 1 to 566)  
 COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Eco RI site shown at the beginning of the sequence.  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 CDNA Library Preparation: M.B. Soares Lab  
 CDNA Library Arrayed by: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/dbtrp/image/image.html  
 Seq primer: M13 Forward.

# FEATURES

source 1..566  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3060360"  
 /tissue\_type="lymph"  
 /cell\_type="germinal center B cells"  
 /cell\_line="MGC85"  
 /lab\_host="DH10B (LTI)"  
 /clone\_lib="NIH\_MGC\_37"  
 /note="Vector: pTZ19-Pac; Site 1: NotI; Site 2: Eco RI;  
 Constructed from size fractionated cytoplasmic mRNA  
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis  
 M. Staudt, Ph.D. Library preparation by Maria de Fátima  
 Bonafide, Ph.D. and M. Bento Soares, Ph.D."  
 BASE COUNT 129 a 169 c 145 g 123 t

Query Match 33.6%; Score 308.6; DB 9; Length 566;  
 Best Local Similarity 93.1%; Pred. No. 5.6e-69;  
 Matches 336; Conservative 0; Mismatches 19; Indels 6; Gaps 1;

Qy 70 GAAATGTGTGACGAGCTCTCCAGGACCTGTCTTTGTCTCCAGGGGAAAGACCACC 129  
 Db 66 GAAATGTGTGACGAGCTCTCCAGGACCTGTCTTTGTCTCCAGGGGAAAGACCACC 125  
 Qy 130 CTCCTCGACGGCCAGTCAAGATTGACGACGACTTACCTTGCTGACGACGAGG 189  
 Db 126 CTCCTCGACGGCCAGTCAAGATTGACGACGACTTACCTTGCTGACGACGAGG 185  
 Qy 190 CCGGACAGGCTCCAGAGCTCTCATCTATGTCATCCACGAGGCCACTGGCATGCCA 249  
 Db 186 CCGGACAGGCTCCAGAGCTCTCATCTATGTCATCCACGAGGCCACTGGCATGCCA 245  
 Qy 250 GACAGGTTCAAGTGGCAGTGGGTCCGGACAGACTTCACTTCACCATCAGTAGACTGGAG 309  
 Db 246 GACAGGTTCAAGTGGCAGTGGGTCTGGGACAGACTTCACTTCACCATCAGTAGAG 305  
 Qy 310 CCGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGTCAGTCACTCAGACCTCGAG 369  
 Db 306 CCGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGTCAGTCACTCAGACCTCGAG 359  
 Qy 370 ATCACTTTGGCGGAGGACCAAGTGGAGATCAACGAACTGTGGCTGCACCATCTGTC 429  
 Db 360 CTCACCTTTGGCGGAGGACCAAGTGGAGATCAACGAACTGTGGCTGCACCATCTGTC 419  
 Qy 430 T 430  
 Db 420 T 420

RESULT 8  
 B1759245 745 bp mRNA linear EST 25-SEP-2001  
 LOCUS B1759245 603042678F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5183010 5',  
 DEFINITION mRNA sequence.  
 ACCESSION B1759245  
 VERSION B1759245.1 GI:15750823  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
 JOURNAL 1 (bases 1 to 745)  
 COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM11456 row: 1 column: 19  
 High quality sequence stop: 724.

# FEATURES

source 1..745  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5183010"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_116"  
 /note="Organ: pooled colon, kidney, stomach; Vector:  
 pCMV-SpRTE; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of 3 colons, age 26 yo male, 49 yo  
 female, 71 yo male colon; 46 yo male kidney, and pool of 2  
 stomachs, 62 yo male and 70 yo female. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.4 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code  
023. Note: this is a NIH\_MGC Library."

BASE COUNT 189 a 219 c 194 g 143 t

Query Match 33.6%; Score 308; DB 12; Length 745;  
Best Local Similarity 85.8%; Pred. No. 9, 2e-69;  
Matches 357; Conservative 0; Mismatches 50; Indels 9; Gaps 1;

ORIGIN  
15 AACCGTATGCGCATGCGCACTGCGTGGTTCCTGCTACCGTGGCCGAGCGCATAT 74  
21 AAACCCGAGCGAGCTTCTCTCTCTGCTGCTGCTCCAGATACCCGAGAGAA 80  
75 TGTGTGACGCACTCTCCAGGACCCGTTTGTGTCCAGGGGAAAGCCACTCTTC 134  
81 TGTGTGAGCACTCTCCAGGACCCGTTTGTGTCCAGGGGAAAGCCACTCTTC 140  
135 CTGACAGGCGCAGTCAAGTGTGTAGTACAGCTAAGCTGTGTACAGAGAACTGG 194  
141 CTGACAGGCGCAGTCAAGTGTGTAGTACAGCTAAGCTGTGTACAGAGAACTGG 200  
195 CCAGGCTCCAGGCTCTCATCTATGTGTATGTCATCCAGAGGCGCATGCGATGCA 254  
201 CCAGGCTCCAGGCTCTCATCTATGTGTATGTCATCCAGAGGCGCATGCGATGCA 260  
255 GTTCAGTGGCAGTGGGTCCGGGACAGACTTCACTCTCACTCAGTACAGTGGAGCC 314  
261 GTTCAGTGGCAGTGGGTCCGGGACAGACTTCACTCTCACTCAGTACAGTGGAGCC 320  
315 AATTTTGCAGTGTATTAATCTGTCAGAGTATGTATGTCAGTACAGTGGAGCC 374  
321 AATTTTGCAGTGTATTAATCTGTCAGAGTATGTATGTCAGTACAGTGGAGCC 371  
375 TTTCGCGGAGGAGCAAGTGGAGTCAAGTGGAGTGGAGTGGAGTGGAGTGGAGT 430  
372 TTTCGCGGAGGAGCAAGTGGAGTCAAGTGGAGTGGAGTGGAGTGGAGTGGAGT 427

RESULT 9  
AV647117 433 bp mRNA linear EST 15-JAN-2002

LOCUS AV647117 GLC Homo sapiens cDNA clone GLCAUH04 3', mRNA sequence.  
DEFINITION AV647117  
ACCESSION AV647117  
VERSION AV647117.1 GI:9868131  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, D., Hu, W., Shen, K., Gu, J., Chen, Z., and Han, Z.  
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

TITLE  
JOURNAL MEDLINE  
PUBMED 21625106  
COMMENT Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China  
Tel: 86-21-50801919 (ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.

FEATURES  
source 1. 433  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"

/clone="GLCAUH04"  
/issue\_type="corresponding non cancerous liver tissue"  
/dev\_stage="adult"  
/lab\_stage="SOLR"  
/lab\_host="SOLR"  
/clone\_id="GLC"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 95 a 127 c 115 g 95 t 1 others

Query Match 33.5%; Score 307.8; DB 9; Length 433;  
Best Local Similarity 93.4%; Pred. No. 8e-69;  
Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

ORIGIN  
70 GATATGTGTGACGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGAGCCACC 129  
83 GAATTTGTGTGACGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGAGCCACC 142  
130 CTCTCTGCGAGGCGCAGTCAAGTGTGTAGTACAGCTAAGCTGTGTACAGAGAA 189  
143 CTCTCTGCGAGGCGCAGTCAAGTGTGTAGTACAGCTAAGCTGTGTACAGAGAA 202  
190 CCGGCGCAGGCTCCAGGCTCTCATCTATGTGTATGTCATCCAGAGGCGCATGCGCA 249  
203 CTTCGCGAGGCTCCAGGCTCTCATCTATGTGTATGTCATCCAGAGGCGCATGCGCA 262  
250 GACAGTTCAGTGGCAGTGGGTCCGGGACAGACTTCACTCTCACTCAGTACAGTGGAG 309  
263 GACAGTTCAGTGGCAGTGGGTCCGGGACAGACTTCACTCTCACTCAGTACAGTGGAG 322  
310 CCTGAAGATTTTGCAGTGTATTAATCTGTCAGAGTATGTATGTCAGTACAGTGGAG 369  
323 CCTGAAGATTTTGCAGTGTATTAATCTGTCAGAGTATGTATGTCAGTACAGTGGAG 371  
370 ATCACTTTGCGGAGGAGCAAGTGGAGTCAAGTGGAGTGGAGTGGAGTGGAGTGGAGT 429  
372 -TCACCTTTGCGGAGGAGCAAGTGGAGTCAAGTGGAGTGGAGTGGAGTGGAGTGGAGT 430  
430 T 430  
431 T 431

RESULT 10  
AV647111

LOCUS AV647111 440 bp mRNA linear EST 15-JAN-2002  
DEFINITION AV647111 GLC Homo sapiens cDNA clone GLCAUH10 3', mRNA sequence.  
ACCESSION AV647111  
VERSION AV647111.1 GI:9868125  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, D., Hu, W., Shen, K., Gu, J., Chen, Z., and Han, Z.  
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

TITLE  
JOURNAL MEDLINE  
PUBMED 21625106  
COMMENT Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China  
Tel: 86-21-50801919 (ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.

FEATURES  
source 1. 433  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"

FEATURES  
Source

Location/Qualifiers  
1..440  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="GLCAUG10"  
/tissue\_type="corresponding non cancerous liver tissue"  
/dev\_stage="Adult"  
/lab\_host="SOLR"  
/clone\_1ib="GLC"  
/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"  
BASE COUNT 96 a 132 c 116 g 95 t 1 others  
ORIGIN

Query Match 33.5%; Score 307.8; DB 9; Length 440;  
Best Local Similarity 93.4%; Pred. No. 8.1e-69;  
Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

70 GATATTGTGTGACGACGCTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGACCAACC 129  
91 GAAATTTGTGTGACGACGCTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGACCAACC 150  
130 CTCTCTGACGGGCGACGTCAGAGTGTAGTACGACGCTTACCTGTGACGACGAGAA 189  
151 CTCTCTGACGGGCGACGTCAGAGTGTAGTACGACGCTTACCTGTGACGACGAGAA 210  
190 CTGAGCGAGGCTCCAGGCTCTCATCTATGCTGATCCACAGGGGCGACCTGGCATGCCA 249  
211 CTGAGCGAGGCTCCAGGCTCTCATCTATGCTGATCCACAGGGGCGACCTGGCATGCCA 270  
250 GACAGGTCAGTGGCAGTGGGTCGGGACAGACTTCACTTCACCATCAGTACGATGGAG 309  
271 GACAGATTCAGTGGCAGTGGGTCGGGACAGACTTCACTTCACCATCAGTACGATGGAG 330  
310 CCTGAAGATTTTGCAGTGTATTACTGTACGACGATAGTGTAGTACCTCAGACACTCAG 369  
331 CCTGAAGATTTTGCAGTGTATTACTGTACGACGATAGTGTAGTACCTCAGACACTCAG 379  
370 ATCACTTTGGCGGCGAGGACCAAGGTGAGATCAAGCACTGTGGCTGACCATCTGTGC 429  
430 T 430  
439 T 439

RESULT 11  
AM405787 504 bp mRNA linear EST 16-FEB-2000  
LOCUS .  
DEFINITION UT-HF-BL0-abp-e-02-0-UT.r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
IMAGE:3057482 5', mRNA sequence.

ACCESSION AM405787  
VERSION AM405787.1 GI:6924844  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
TITLE NIH-MGC http://mgi.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: M.B. Soares Lab  
CDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

FEATURES  
Source

www.bio.lnl.gov/bbrp/image/image.html  
Seq primer: M13 Forward.  
Location/Qualifiers  
1..504  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3057482"  
/tissue\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LTI)"  
/clone\_1ib="NIH\_MGC\_37"  
/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(1.5-2.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonfido, Ph.D. and W. Bento Soares, Ph.D."  
BASE COUNT 117 a 147 c 127 g 113 t  
ORIGIN

Query Match 33.5%; Score 307.8; DB 9; Length 504;  
Best Local Similarity 93.4%; Pred. No. 8.6e-69;  
Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

70 GATATTGTGTGACGACGCTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGACCAACC 129  
74 GAAATTTGTGTGACGACGCTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGACCAACC 133  
130 CTCTCTGACGGGCGACGTCAGAGTGTAGTACGACGCTTACCTGTGACGACGAGAA 189  
134 CTCTCTGACGGGCGACGTCAGAGTGTAGTACGACGCTTACCTGTGACGACGAGAA 193  
190 CTGAGCGAGGCTCCAGGCTCTCATCTATGCTGATCCACAGGGGCGACCTGGCATGCCA 249  
194 CTGAGCGAGGCTCCAGGCTCTCATCTATGCTGATCCACAGGGGCGACCTGGCATGCCA 253  
250 GACAGGTCAGTGGCAGTGGGTCGGGACAGACTTCACTTCACCATCAGTACGATGGAG 309  
254 GACAGATTCAGTGGCAGTGGGTCGGGACAGACTTCACTTCACCATCAGTACGATGGAG 313  
310 CCTGAAGATTTTGCAGTGTATTACTGTACGACGATAGTGTAGTACCTCAGACACTCAG 369  
314 CCTGAAGATTTTGCAGTGTATTACTGTACGACGATAGTGTAGTACCTCAGACACTCAG 364  
370 ATCACTTTGGCGGCGAGGACCAAGGTGAGATCAAGCACTGTGGCTGACCATCTGTGC 429  
365 --ACGTTGGCGGCGAGGACCAAGGTGAGATCAAGCACTGTGGCTGACCATCTGTGC 421  
430 T 430  
422 T 422

RESULT 12  
BG686748 734 bp mRNA linear EST 01-MAY-2001  
LOCUS .  
DEFINITION 602650717P1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4763021 5',  
mRNA sequence.

ACCESSION BG686748  
VERSION BG686748.1 GI:13918145  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
TITLE NIH-MGC http://mgi.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
 Plate: L1CML618 row: a column: 06  
 High quality sequence stop: 709.  
 Location/Qualifiers  
 1..734

FEATURES  
 source  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4763021"  
 /tissue\_type="Primary B-cells from tonsils (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_48"  
 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the Laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH MGC Library."  
 BASE COUNT 184 a 217 c 191 g 142 t  
 ORIGIN

Query Match 33.5%; Score 307.8; DB 10; Length 734;  
 Best Local Similarity 93.4%; Pred. No. 1e-68;  
 Matches 33/7; Conservative 0; Mismatches 12; Indels 12; Gaps 1;  
 QY 70 GATATGTGTGACGACGCTCCAGGACCCCTGCTTCTCCAGGGGAAAGCCACC 129  
 |||  
 DB 67 GAATTTGTGTGACGACGCTCCAGGACCCCTGCTTCTCCAGGGGAAAGCCACC 126  
 |||  
 QY 130 CTCTCTGACAGGGCCAGTCAAGTGTAGTAGCAGTACTTACCTGTGACAGAGAA 189  
 |||  
 DB 127 CTCTCTGACAGGGCCAGTCAAGTGTAGTAGCAGTACTTACCTGTGACAGAGAA 186  
 |||  
 QY 190 CTTGGCCAGGGCTCCAGGCTCTCATTTATGTGATCCACAGGGCCACTGGCATGCCA 249  
 |||  
 DB 187 CTTGGCCAGGGCTCCAGGCTCTCATTTATGTGATCCACAGGGCCACTGGCATGCCA 246  
 |||  
 QY 250 GACAGGTTCACTGAGTGGATCCGGGACAGACTTCACTCCATCAGAGGCTGAG 309  
 |||  
 DB 247 GACAGGTTCACTGAGTGGATCCGGGACAGACTTCACTCCATCAGAGGCTGAG 306  
 |||  
 QY 310 CTTGAAGATTTTGCAGTATTAATCTGTCAAGAGTATGTAGTCACTCAGACACTCCAG 369  
 |||  
 DB 307 CTTGAAGATTTTGCAGTATTAATCTGTCAAGAGTATGTAGTCACTCAGACACTCCAG 357  
 |||  
 QY 370 ATGACTTTGGGGGAGGACCAAGGTGAGATCAAAAGAACTGTGGCTGACCATCTGTC 429  
 |||  
 DB 358 ---ACGTTGGCCAGGAGCAAGGTGAGAAATCAAGAACTGTGGCTGACCATCTGTC 414  
 |||  
 QY 430 T 430  
 |||  
 DB 415 T 415

RESULT 13  
 AV646708 793 bp mRNA 1linear EST 15-JAN-2002  
 LOCUS AV646708 GJC Homo sapiens cDNA clone GJCAG001.3, mRNA sequence.  
 DEFINITION AV646708  
 ACCESSION AV646708  
 VERSION AV646708.1 GI:9867722  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 AUTHORS  
 1 (bases 1 to 793)  
 Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,  
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,  
 Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,  
 Hu, G., Gu, J., Chen, Z., and Han, Z.  
 Insight into hepatocellular carcinogenesis at transcriptome level  
 by comparing gene expression profiles of hepatocellular carcinoma  
 with those of corresponding noncancerous liver  
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)  
 MEDLINE  
 PUBMED  
 11752456  
 COMMENT  
 Contact: Zeguang Han  
 Chinese National Human Genome Center at Shanghai  
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
 201203, P. R. China  
 Tel: 86-21-50801919 (ex.45)  
 Fax: 86-21-50801922  
 Email: hanzg@hgsc.sh.cn  
 This clone is available at CHGC in Shanghai.  
 FEATURES  
 source  
 1..793  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="GJCAG001"  
 /tissue\_type="corresponding non cancerous liver tissue"  
 /dev\_stage="Adult"  
 /lab\_host="SOIR"  
 /clone\_lib="GLC"  
 /note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2:  
 XhoI"

BASE COUNT 185 a 234 c 201 g 162 t 11 others  
 ORIGIN

Query Match 33.5%; Score 307.8; DB 9; Length 793;  
 Best Local Similarity 93.4%; Pred. No. 1.1e-68;  
 Matches 33/7; Conservative 0; Mismatches 12; Indels 12; Gaps 1;  
 QY 70 GATATGTGTGACGACGCTCCAGGACCCCTGCTTCTCCAGGGGAAAGCCACC 129  
 |||  
 DB 57 GAATTTGTGTGACGACGCTCCAGGACCCCTGCTTCTCCAGGGGAAAGCCACC 116  
 |||  
 QY 130 CTCTCTGACAGGGCCAGTCAAGTGTAGTAGCAGTACTTACCTGTGACAGAGAA 189  
 |||  
 DB 117 CTCTCTGACAGGGCCAGTCAAGTGTAGTAGCAGTACTTACCTGTGACAGAGAA 176  
 |||  
 QY 190 CTTGGCCAGGGCTCCAGGCTCTCATTTATGTGATCCACAGGGCCACTGGCATGCCA 249  
 |||  
 DB 177 CTTGGCCAGGGCTCCAGGCTCTCATTTATGTGATCCACAGGGCCACTGGCATGCCA 236  
 |||  
 QY 250 GACAGGTTCACTGAGTGGATCCGGGACAGACTTCACTCCATCAGAGGCTGAG 309  
 |||  
 DB 237 GACAGGTTCACTGAGTGGATCCGGGACAGACTTCACTCCATCAGAGGCTGAG 296  
 |||  
 QY 310 CTTGAAGATTTTGCAGTATTAATCTGTCAAGAGTATGTAGTCACTCAGACACTCCAG 369  
 |||  
 DB 297 CTTGAAGATTTTGCAGTATTAATCTGTCAAGAGTATGTAGTCACTCAGACACTCCAG 345  
 |||  
 QY 370 ATGACTTTGGGGGAGGACCAAGGTGAGATCAAAAGAACTGTGGCTGACCATCTGTC 429  
 |||  
 DB 346 -TCACTTTGGGGGAGGACCAAGGTGAGATCAAAAGAACTGTGGCTGACCATCTGTC 404  
 |||  
 QY 430 T 430  
 |||  
 DB 405 T 405

RESULT 14  
 BQ706634 926 bp mRNA 1linear EST 16-JUN-2002  
 LOCUS BQ706634  
 DEFINITION BQ706634 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6215094  
 ACCESSION BQ706634  
 5', mRNA sequence.



```

VERSION      B0706634.1  GI:21845533
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS      NIH-MGC http://mhc.nci.nih.gov/
TITLE        NIH-MGC
JOURNAL      Unpublished
COMMENT      Contact: Robert Strusberg, Ph.D.
              Email: cga@bbs-remail.nih.gov
              Tissue Procurement: Dr. Mark Watson
              CDNA Library Preparation: Rubin Laboratory
              DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.llnl.gov
              Plate: LNCM2383 row: h column: 07
              High quality sequence stop: 536.
              Location/Qualifiers
                1..926
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:6215094"
                  /lab_host="DH10B (phage-resistant)"
                  /clone_lib="NIH-MGC_113"
                  /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                  EcoRI; CDNA made by oligo-dT priming. Directionally cloned
                  into EcoRI/XhoI sites using the following 5' adaptor:
                  GGACGAG(G). Library constructed by Ling Hong in the
                  laboratory of Gerald M. Rubin (University of California,
                  Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
                  Superscript II RT (Life Technologies). Note: this is a
                  NIH MGC library."
BASE COUNT   213 a 278 c 239 g 196 t
ORIGIN
Query Match      33.5%; Score 307.8; DB 13; Length 926;
Best Local Similarity 93.4%; Pred. No. 1.1e-68;
Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;
QY 70 GATATTGTTGAGCGAGCTCCAGGACCCCTGTGTCTCCAGGGGAAGGCCACC 129
DB 67 GAAATTGTTGAGCGAGCTCCAGGACCCCTGTGTCTCCAGGGGAAGGCCACC 126
QY 130 CTCTCTCAGGGGCGAGTCAAGATGTTAGTACAGCTTACCTGTGACGAGAA 189
DB 127 CTCTCTCAGGGGCGAGTCAAGATGTTAGTACAGCTTACCTGTGACGAGAA 186
QY 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGCTGATCCAGGAGGCACTGGCATGCCA 249
DB 187 CTTGGCCAGGCTCCAGGCTCTCATCTATGCTGATCCAGGAGGCACTGGCATGCCA 246
QY 250 GACAGTTCAAGTGGAGAGGCTCCGAGACAGCTTCACTTCACATCAGTGAAGCTGGAG 309
DB 247 GACAGTTCAAGTGGAGAGGCTCCGAGACAGCTTCACTTCACATCAGTGAAGCTGGAG 306
QY 310 CTTGAAGATTTTGCAGTGTATTACTGTACAGAGTATGTAAGCTCACTCAGACCTCGAG 369
DB 307 CTTGAAGATTTTGCAGTGTATTACTGTACAGAGTATGTAAGCTCACTCAGACCTCGAG 364
QY 370 ATCACTTTGGCGGAGGACCAAGGTGAGATCAAGCAAGTGTGGCTGCACCATCTGTC 429
DB 355 CTCACCTTTGGCGGAGGACCAAGGTGAGATCAAGCAAGTGTGGCTGCACCATCTGTC 414
QY 430 T 430
DB 415 T 415

```

```

RESULT 15
B0709245
LOCUS      998 bp mRNA linear EST 16-JUL-2002
DEFINITION AGNCOURT 7975569 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6214925
              5', mRNA sequence.
ACCESSION  B0709245
VERSION    B0709245
KEYWORDS   B0709245.1 GI:21848144
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS     NIH-MGC http://mhc.nci.nih.gov/
TITLE       NIH-MGC
JOURNAL     Unpublished
COMMENT     Contact: Robert Strusberg, Ph.D.
              Email: cga@bbs-remail.nih.gov
              Tissue Procurement: Dr. Mark Watson
              CDNA Library Preparation: Rubin Laboratory
              DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.llnl.gov
              Plate: LNCM2383 row: a column: 06
              High quality sequence stop: 500.
              Location/Qualifiers
                1..998
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:6214925"
                  /lab_host="DH10B (phage-resistant)"
                  /clone_lib="NIH-MGC_113"
                  /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                  EcoRI; CDNA made by oligo-dT priming. Directionally cloned
                  into EcoRI/XhoI sites using the following 5' adaptor:
                  GGACGAG(G). Library constructed by Ling Hong in the
                  laboratory of Gerald M. Rubin (University of California,
                  Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
                  Superscript II RT (Life Technologies). Note: this is a
                  NIH MGC library."
BASE COUNT   240 a 290 c 265 g 203 t
ORIGIN
Query Match      33.5%; Score 307.8; DB 13; Length 998;
Best Local Similarity 93.4%; Pred. No. 1.2e-68;
Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;
QY 70 GATATTGTTGAGCGAGCTCCAGGACCCCTGTGTCTCCAGGGGAAGGCCACC 129
DB 66 GAAATTGTTGAGCGAGCTCCAGGACCCCTGTGTCTCCAGGGGAAGGCCACC 125
QY 130 CTCTCTCAGGGGCGAGTCAAGATGTTAGTACAGCTTACCTGTGACGAGAA 189
DB 126 CTCTCTCAGGGGCGAGTCAAGATGTTAGTACAGCTTACCTGTGACGAGAA 185
QY 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGCTGATCCAGGAGGCACTGGCATGCCA 249
DB 186 CTTGGCCAGGCTCCAGGCTCTCATCTATGCTGATCCAGGAGGCACTGGCATGCCA 245
QY 250 GACAGTTCAAGTGGAGAGGCTCCGAGACAGCTTCACTTCACATCAGTGAAGCTGGAG 309
DB 246 GACAGTTCAAGTGGAGAGGCTCCGAGACAGCTTCACTTCACATCAGTGAAGCTGGAG 305
QY 310 CTTGAAGATTTTGCAGTGTATTACTGTACAGAGTATGTAAGCTCACTCAGACCTCGAG 369
DB 306 CTTGAAGATTTTGCAGTGTATTACTGTACAGAGTATGTAAGCTCACTCAGACCTCGAG 363
QY 370 ATCACTTTGGCGGAGGACCAAGGTGAGATCAAGCAAGTGTGGCTGCACCATCTGTC 429
DB 354 CTCACCTTTGGCGGAGGACCAAGGTGAGATCAAGCAAGTGTGGCTGCACCATCTGTC 413

```

Qy	430 T 430
Db	414 T 414

Search completed: September 17, 2003, 04:21:49  
Job time : 1938 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 03:02:49 ; Search time 2893 Seconds  
(without alignments)  
10523.453 Million cell updates/sec

Title: US-08-657-449-13

Perfect score: 918  
Sequence: 1 GAATTCATGAAAAAACC...ATCACCATTAAGTGAAGCTT 918

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 3336368 seqs, 1658189874 residues

Total number of hits satisfying chosen parameters: 66727376

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: Pending\_Patents\_NA\_Main.\*
- 2: /cgn2\_6/ptodata/2/pna/PCTUS\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/pna/US06\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/pna/US07\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/pna/US081\_COMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pna/US082\_COMB.seq.\*
- 8: /cgn2\_6/ptodata/2/pna/US083\_COMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pna/US084\_COMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pna/US085\_COMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pna/US086\_COMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pna/US087\_COMB.seq.\*
- 13: /cgn2\_6/ptodata/2/pna/US088\_COMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pna/US089\_COMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pna/US090\_COMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pna/US091\_COMB.seq.\*
- 17: /cgn2\_6/ptodata/2/pna/US092\_COMB.seq.\*
- 18: /cgn2\_6/ptodata/2/pna/US092B\_COMB.seq.\*
- 19: /cgn2\_6/ptodata/2/pna/US093A\_COMB.seq.\*
- 20: /cgn2\_6/ptodata/2/pna/US093B\_COMB.seq.\*
- 21: /cgn2\_6/ptodata/2/pna/US094\_COMB.seq.\*
- 22: /cgn2\_6/ptodata/2/pna/US095A\_COMB.seq.\*
- 23: /cgn2\_6/ptodata/2/pna/US095B\_COMB.seq.\*
- 24: /cgn2\_6/ptodata/2/pna/US095C\_COMB.seq.\*
- 25: /cgn2\_6/ptodata/2/pna/US095D\_COMB.seq.\*
- 26: /cgn2\_6/ptodata/2/pna/US096A\_COMB.seq.\*
- 27: /cgn2\_6/ptodata/2/pna/US096B\_COMB.seq.\*
- 28: /cgn2\_6/ptodata/2/pna/US096C\_COMB.seq.\*
- 29: /cgn2\_6/ptodata/2/pna/US096D\_COMB.seq.\*
- 30: /cgn2\_6/ptodata/2/pna/US096E\_COMB.seq.\*
- 31: /cgn2\_6/ptodata/2/pna/US097A\_COMB.seq.\*
- 32: /cgn2\_6/ptodata/2/pna/US097B\_COMB.seq.\*
- 33: /cgn2\_6/ptodata/2/pna/US097C\_COMB.seq.\*
- 34: /cgn2\_6/ptodata/2/pna/US098A\_COMB.seq.\*
- 35: /cgn2\_6/ptodata/2/pna/US098B\_COMB.seq.\*
- 36: /cgn2\_6/ptodata/2/pna/US098C\_COMB.seq.\*
- 37: /cgn2\_6/ptodata/2/pna/US098D\_COMB.seq.\*
- 38: /cgn2\_6/ptodata/2/pna/US099A\_COMB.seq.\*
- 39: /cgn2\_6/ptodata/2/pna/US099B\_COMB.seq.\*
- 40: /cgn2\_6/ptodata/2/pna/US099C\_COMB.seq.\*
- 41: /cgn2\_6/ptodata/2/pna/US099D\_COMB.seq.\*
- 42: /cgn2\_6/ptodata/2/pna/US099E\_COMB.seq.\*
- 43: /cgn2\_6/ptodata/2/pna/US099F\_COMB.seq.\*

- 44: /cgn2\_6/ptodata/2/pna/US100A\_COMB.seq.\*
- 45: /cgn2\_6/ptodata/2/pna/US100B\_COMB.seq.\*
- 46: /cgn2\_6/ptodata/2/pna/US101A\_COMB.seq.\*
- 47: /cgn2\_6/ptodata/2/pna/US101B\_COMB.seq.\*
- 48: /cgn2\_6/ptodata/2/pna/US102A\_COMB.seq.\*
- 49: /cgn2\_6/ptodata/2/pna/US102B\_COMB.seq.\*
- 50: /cgn2\_6/ptodata/2/pna/US103A\_COMB.seq.\*
- 51: /cgn2\_6/ptodata/2/pna/US103B\_COMB.seq.\*
- 52: /cgn2\_6/ptodata/2/pna/US104A\_COMB.seq.\*
- 53: /cgn2\_6/ptodata/2/pna/US104B\_COMB.seq.\*
- 54: /cgn2\_6/ptodata/2/pna/US6000\_COMB.seq.\*
- 55: /cgn2\_6/ptodata/2/pna/US6001\_COMB.seq.\*
- 56: /cgn2\_6/ptodata/2/pna/US6002\_COMB.seq.\*
- 57: /cgn2\_6/ptodata/2/pna/US6003\_COMB.seq.\*
- 58: /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq.\*
- 59: /cgn2\_6/ptodata/2/pna/US6005\_COMB.seq.\*
- 60: /cgn2\_6/ptodata/2/pna/US6006\_COMB.seq.\*
- 61: /cgn2\_6/ptodata/2/pna/US6007\_COMB.seq.\*
- 62: /cgn2\_6/ptodata/2/pna/US6008\_COMB.seq.\*
- 63: /cgn2\_6/ptodata/2/pna/US6009\_COMB.seq.\*
- 64: /cgn2\_6/ptodata/2/pna/US6010\_COMB.seq.\*
- 65: /cgn2\_6/ptodata/2/pna/US6011\_COMB.seq.\*
- 66: /cgn2\_6/ptodata/2/pna/US6012\_COMB.seq.\*
- 67: /cgn2\_6/ptodata/2/pna/US6013\_COMB.seq.\*
- 68: /cgn2\_6/ptodata/2/pna/US6014\_COMB.seq.\*
- 69: /cgn2\_6/ptodata/2/pna/US6015\_COMB.seq.\*
- 70: /cgn2\_6/ptodata/2/pna/US6016\_COMB.seq.\*
- 71: /cgn2\_6/ptodata/2/pna/US6017\_COMB.seq.\*
- 72: /cgn2\_6/ptodata/2/pna/US6018\_COMB.seq.\*
- 73: /cgn2\_6/ptodata/2/pna/US6019\_COMB.seq.\*
- 74: /cgn2\_6/ptodata/2/pna/US6020\_COMB.seq.\*
- 75: /cgn2\_6/ptodata/2/pna/US6021\_COMB.seq.\*
- 76: /cgn2\_6/ptodata/2/pna/US6022\_COMB.seq.\*
- 77: /cgn2\_6/ptodata/2/pna/US6023\_COMB.seq.\*
- 78: /cgn2\_6/ptodata/2/pna/US6023B\_COMB.seq.\*
- 79: /cgn2\_6/ptodata/2/pna/US6024\_COMB.seq.\*
- 80: /cgn2\_6/ptodata/2/pna/US6025\_COMB.seq.\*
- 81: /cgn2\_6/ptodata/2/pna/US6026\_COMB.seq.\*
- 82: /cgn2\_6/ptodata/2/pna/US6027\_COMB.seq.\*
- 83: /cgn2\_6/ptodata/2/pna/US6028\_COMB.seq.\*
- 84: /cgn2\_6/ptodata/2/pna/US6029\_COMB.seq.\*
- 85: /cgn2\_6/ptodata/2/pna/US6030\_COMB.seq.\*
- 86: /cgn2\_6/ptodata/2/pna/US6031\_COMB.seq.\*
- 87: /cgn2\_6/ptodata/2/pna/US6032\_COMB.seq.\*
- 88: /cgn2\_6/ptodata/2/pna/US6033\_COMB.seq.\*
- 89: /cgn2\_6/ptodata/2/pna/US6034\_COMB.seq.\*
- 90: /cgn2\_6/ptodata/2/pna/US6035\_COMB.seq.\*
- 91: /cgn2\_6/ptodata/2/pna/US6036\_COMB.seq.\*
- 92: /cgn2\_6/ptodata/2/pna/US6037\_COMB.seq.\*
- 93: /cgn2\_6/ptodata/2/pna/US6038\_COMB.seq.\*
- 94: /cgn2\_6/ptodata/2/pna/US6039\_COMB.seq.\*
- 95: /cgn2\_6/ptodata/2/pna/US6040\_COMB.seq.\*
- 96: /cgn2\_6/ptodata/2/pna/US6041\_COMB.seq.\*
- 97: /cgn2\_6/ptodata/2/pna/US6042\_COMB.seq.\*
- 98: /cgn2\_6/ptodata/2/pna/US6043\_COMB.seq.\*
- 99: /cgn2\_6/ptodata/2/pna/US6044\_COMB.seq.\*
- 100: /cgn2\_6/ptodata/2/pna/US6045\_COMB.seq.\*
- 101: /cgn2\_6/ptodata/2/pna/US6046\_COMB.seq.\*
- 102: /cgn2\_6/ptodata/2/pna/US6047\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	918	100.0	918	11	US-08-657-449-13
2	918	100.0	918	30	US-09-697-561-13
3	918	100.0	918	30	US-09-697-561A-13
4	918	100.0	918	33	US-09-782-397-13

5	118	100.0	918	33	US-09-782-397A-13	Sequence 13, Appl
6	918	100.0	918	33	US-09-782-397B-13	Sequence 13, Appl
7	918	100.0	918	33	US-09-782-397C-13	Sequence 13, Appl
8	916.4	99.8	918	11	US-08-657-449-15	Sequence 15, Appl
9	916.4	99.8	918	30	US-09-697-561-15	Sequence 15, Appl
10	916.4	99.8	918	30	US-09-697-561A-15	Sequence 15, Appl
11	916.4	99.8	918	33	US-09-782-397-15	Sequence 15, Appl
12	916.4	99.8	918	33	US-09-782-397A-15	Sequence 15, Appl
13	916.4	99.8	918	33	US-09-782-397B-15	Sequence 15, Appl
14	916.4	99.8	918	33	US-09-782-397C-15	Sequence 15, Appl
15	799.6	87.1	867	11	US-08-657-449-16	Sequence 16, Appl
16	799.6	87.1	867	30	US-09-697-561-16	Sequence 16, Appl
17	799.6	87.1	867	30	US-09-697-561A-16	Sequence 16, Appl
18	799.6	87.1	867	33	US-09-782-397-16	Sequence 16, Appl
19	799.6	87.1	867	33	US-09-782-397A-16	Sequence 16, Appl
20	799.6	87.1	867	33	US-09-782-397B-16	Sequence 16, Appl
21	799.6	87.1	867	33	US-09-782-397C-16	Sequence 16, Appl
22	798	86.9	867	11	US-08-657-449-18	Sequence 18, Appl
23	798	86.9	867	30	US-09-697-561-18	Sequence 18, Appl
24	798	86.9	867	30	US-09-697-561A-18	Sequence 18, Appl
25	798	86.9	867	33	US-09-782-397-18	Sequence 18, Appl
26	798	86.9	867	33	US-09-782-397A-18	Sequence 18, Appl
27	798	86.9	867	33	US-09-782-397B-18	Sequence 18, Appl
28	798	86.9	867	33	US-09-782-397C-18	Sequence 18, Appl
29	445	44.5	1630	32	US-09-744-625A-36	Sequence 36, Appl
30	445	44.5	1630	32	US-09-744-625A-36	Sequence 36, Appl
31	395.2	43.1	840	1	PCT-US03-10865-20	Sequence 20, Appl
32	395.2	43.1	840	2	PCT-US03-10865-20	Sequence 20, Appl
33	395.2	43.1	840	52	US-10-409-938-20	Sequence 20, Appl
34	361	39.3	450	11	US-08-657-449-6	Sequence 6, Appl
35	361	39.3	450	30	US-09-697-561-6	Sequence 6, Appl
36	361	39.3	450	30	US-09-697-561A-6	Sequence 6, Appl
37	361	39.3	450	33	US-09-782-397-6	Sequence 6, Appl
38	361	39.3	450	33	US-09-782-397A-6	Sequence 6, Appl
39	361	39.3	450	33	US-09-782-397B-6	Sequence 6, Appl
40	361	39.3	450	33	US-09-782-397C-6	Sequence 6, Appl
41	359.4	39.2	450	11	US-08-657-449-4	Sequence 4, Appl
42	359.4	39.2	450	30	US-09-697-561-4	Sequence 4, Appl
43	359.4	39.2	450	30	US-09-697-561A-4	Sequence 4, Appl
44	359.4	39.2	450	33	US-09-782-397-4	Sequence 4, Appl
45	359.4	39.2	450	33	US-09-782-397A-4	Sequence 4, Appl

## ALIGNMENTS

```

1      RESULT 1
2      US-08-657-449-13
3      ; Sequence 13, Application US/08657449
4      ; GENERAL INFORMATION:
5      ; APPLICANT: Dan, Michael D.
6      ; APPLICANT: Maitli, Pradiip K.
7      ; APPLICANT: Kaplan, Howard A.
8      ; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT
9      ; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
10     ; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
11     ; TITLE OF INVENTION: DETECTION OF CANCERS
12     ; NUMBER OF SEQUENCES: 18
13     ; CORRESPONDENCE ADDRESS:
14     ; ADDRESSEE: Morrison & Foerster
15     ; STREET: 755 Page Mill Road
16     ; CITY: Palo Alto
17     ; STATE: CA
18     ; COUNTRY: USA
19     ; ZIP: 94304-1018
20     ; COMPUTER READABLE FORM:
21     ; MEDIUM TYPE: Floppy disk
22     ; COMPUTER: IBM PC compatible
23     ; OPERATING SYSTEM: PC-DOS/MS-DOS
24     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
25     ; CURRENT APPLICATION DATA:
26     ; APPLICATION NUMBER: US/08/657,449
27     ; FILING DATE:

```

```

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ. ID NO.: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..906, 913..918)
US-08-657-449-13

```

Query Match	100.0%	Score 918;	DB 11;	Length 918;
Best Local Similarity	100.0%	Pred. No. 2.5e-225;		
Matches 918; Conservative	0;	Mismatches	0;	Gaps 0;

Qy		GAATTCATGAAAAAACC	GCTATCGCATG	CAGATTGCA	CTGGCTGGTTTCG	TACAGGTT	60
Db	1	GAATTCATGAAAAAACC	GCTATCGCATG	CAGATTGCA	CTGGCTGGTTTCG	TACAGGTT	60
Qy		GCGCAGGCGCATATTT	GTGTGA	CGCAGTCTTC	CAAGCACCCTCTT	TGTCTCAAGGGAA	120
Db	61	GCGCAGGCGCATATTT	GTGTGA	CGCAGTCTTC	CAAGCACCCTCTT	TGTCTCAAGGGAA	120
Qy		AGAGCCACCCTCTTC	TGCAAGGACAGT	CAGAGTTT	GTGATGACACTT	AGCTAGCTGGTAC	180
Db	121	AGAGCCACCCTCTTC	TGCAAGGACAGT	CAGAGTTT	GTGATGACACTT	AGCTAGCTGGTAC	180
Qy		CAGCAGAAACCTTG	CCAGGCTCC	CAGGCTCTC	TATCTATGATGATC	CACAGGGCCACT	240
Db	181	CAGCAGAAACCTTG	CCAGGCTCC	CAGGCTCTC	TATCTATGATGATC	CACAGGGCCACT	240
Qy		GGCATGCGACACAG	GTTCAGTGCAGTGGGATCC	GGGACAACTTCA	CTCCACCATAGT		300
Db	241	GGCATGCGACACAG	GTTCAGTGCAGTGGGATCC	GGGACAACTTCA	CTCCACCATAGT		300
Qy		GGCATGCGACACAG	GTTCAGTGCAGTGGGATCC	GGGACAACTTCA	CTCCACCATAGT		300
Db	241	GGCATGCGACACAG	GTTCAGTGCAGTGGGATCC	GGGACAACTTCA	CTCCACCATAGT		300
Qy		AGA	CTGAGGCTGAGAATTT	TGCAGTGTATTA	CTGTACAGATATG	TGATGCTCACTCAG	360
Db	301	AGA	CTGAGGCTGAGAATTT	TGCAGTGTATTA	CTGTACAGATATG	TGATGCTCACTCAG	360
Qy		AGACTGGAAGCTG	GAATTTTG	CAGTGTATTA	CTGTACAGATATG	TGATGCTCACTCAG	360
Db	301	AGACTGGAAGCTG	GAATTTTG	CAGTGTATTA	CTGTACAGATATG	TGATGCTCACTCAG	360
Qy		ACACCTCAATCACTT	TTCGGCGAGAGGACCA	AGGTGAAATCAA	CGAACA	CTTGGCGTCGA	420
Db	361	ACACCTCAATCACTT	TTCGGCGAGAGGACCA	AGGTGAAATCAA	CGAACA	CTTGGCGTCGA	420
Qy		CCATCTGCTCTCG	CGGTGCGGTTCC	GGAGTGTGATCA	GAGTGGAGGTG	GCTCCAG	480
Db	421	CCATCTGCTCTCG	CGGTGCGGTTCC	GGAGTGTGATCA	GAGTGGAGGTG	GCTCCAG	480
Qy		GTGCACTGTGTGA	AGTTTG	GGGGAGAGTGTGTCA	AGCTGGAGGTCC	CTTGACACTTCC	540
Db	481	GTGCACTGTGTGA	AGTTTG	GGGGAGAGTGTGTCA	AGCTGGAGGTCC	CTTGACACTTCC	540
Qy		TGTGACACTCTT	GGATTC	CCCTTCAGAAAGTTTG	CTATGCACTGGAGTCC	CGACAGGCTCTA	600
Db	541	TGTGACACTCTT	GGATTC	CCCTTCAGAAAGTTTG	CTATGCACTGGAGTCC	CGACAGGCTCTA	600
Qy		GGCAGAGGGGCTG	AGTGGTGGCAGTTAAT	TCATATGATGAA	AGACTAAATATTA	CTACGCA	660
Db	601	GGCAGAGGGGCTG	AGTGGTGGCAGTTAAT	TCATATGATGAA	AGACTAAATATTA	CTACGCA	660
Qy		GACTCCGTGAAAGG	GCAGTTCA	CCATCTCAGAGACA	CTTCCAAAGACAGG	GTATCTA	720
Db	661	GACTCCGTGAAAGG	GCAGTTCA	CCATCTCAGAGACA	CTTCCAAAGACAGG	GTATCTA	720
Qy		AAATGAAACGCTG	AGACTGAGACACAG	CGCTGTCTAATTA	CTGTGGAGAGATCA	AGC	780
Db	721	AAATGAAACGCTG	AGACTGAGACACAG	CGCTGTCTAATTA	CTGTGGAGAGATCA	AGC	780

Db 721 AAAATGAAGCTTGAAGCTGAGACGAGCTGTCTATTACTGTGAGAGATCAGAGC 780  
 Qy 781 CTGTTGGGTGATGATGACCACTACTACGTTTGGAGCTGTGGGCAAAAGGACCAAGTTC 840  
 Db 781 CTGTTGGGTGATGATGACCACTACTACGTTTGGAGCTGTGGGCAAAAGGACCAAGTTC 840  
 Qy 841 ACCGTCCTCTCAGATCCGAAACAAAACCTGATCAGGAGAGATTTGAAACCATCAACAT 900  
 Db 841 ACCGTCCTCTCAGATCCGAAACAAAACCTGATCAGGAGAGATTTGAAACCATCAACAT 900  
 Qy 901 CACCATTAAGTAAGCTT 918  
 Db 901 CACCATTAAGTAAGCTT 918

# RESULT 2 US-09-697-561-13

; Sequence 13, Application US/09697561

; GENERAL INFORMATION:

; APPLICANT: Dan, Michael D.  
 ; Maiti, Pradip K.

; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT  
 ; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
 ; FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
 ; DETECTION OF CANCERS

; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morrison & Foerster LLP  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto

; STATE: CA  
 ; COUNTRY: USA

; ZIP: 94304-1018  
 ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/697,561  
 ; FILING DATE: 26-Oct-2000

; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/862,124  
 ; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Leinhardt, Susan K.

; REGISTRATION NUMBER: 33,943  
 ; REFERENCE/DOCKET NUMBER: 31608-20001.20

; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 813-5600

; TELEFAX: (650) 494-0792  
 ; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:

; LENGTH: 918 base pairs  
 ; TYPE: nucleic acid

; STRANDEDNESS: single  
 ; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: CDS  
 ; LOCATION: join(1..906, 913..918)

; SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
 ; US-09-697-561-13

Query Match 100.0%; Score 918; DB 30; Length 918;  
 Best Local Similarity 100.0%; Pred. No. 2,5e-225;  
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCATGAAAAAACCCTATCCGATCGCAGTTGCACTGCTGCTGCTTCCCTACCGTT 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 GAATTCATGAAAAAACCCTATCCGATCGCAGTTGCACTGCTGCTGCTTCCCTACCGTT 60  
 Qy 61 GCGCAGCCCGATATTGTGTGACGAGTCTCCAGGCAACCTGCTCTTGTCTCCAGGGAAA 120  
 Db 61 GCGCAGCCCGATATTGTGTGACGAGTCTCCAGGCAACCTGCTCTTGTCTCCAGGGAAA 120  
 Qy 121 AGAGCCACCCTCTCTGCAAGGCGCAGTCAAGTGTGTTAGTAGAGCTACTTACCTGTGAC 180  
 Db 121 AGAGCCACCCTCTCTGCAAGGCGCAGTCAAGTGTGTTAGTAGAGCTACTTACCTGTGAC 180  
 Qy 181 CAGCAAAAACCTGGGCAAGGCTCCAGGCTCCATCTAATGTGATCCACAGGCGCACT 240  
 Db 181 CAGCAAAAACCTGGGCAAGGCTCCAGGCTCCATCTAATGTGATCCACAGGCGCACT 240  
 Qy 241 GCGATCCAGACAGGCTCAGTGGAGTGGGTCGCGGACAGCTTCACTCTCCATCACT 300  
 Db 241 GCGATCCAGACAGGCTCAGTGGAGTGGGTCGCGGACAGCTTCACTCTCCATCACT 300  
 Qy 301 AGACTGAGCCCTGAAAGATTTTGCAGTGTATTACTGTCAAGCAGTATGTAGTCACTCAG 360  
 Db 301 AGACTGAGCCCTGAAAGATTTTGCAGTGTATTACTGTCAAGCAGTATGTAGTCACTCAG 360  
 Qy 361 ACACCTCAGATCACTTTGCGCGAGGACCAAGGTGAGATCAAAACGAACTGTGCTGCA 420  
 Db 361 ACACCTCAGATCACTTTGCGCGAGGACCAAGGTGAGATCAAAACGAACTGTGCTGCA 420  
 Qy 421 CCATCTGCTCTGCGGAGTGGCGGCTCCGAGGAGTGTGATCAGGTGAGAGTGGCTCCAG 480  
 Db 421 CCATCTGCTCTGCGGAGTGGCGGCTCCGAGGAGTGTGATCAGGTGAGAGTGGCTCCAG 480  
 Qy 481 GTGCACTGTGAGATCTGGGAGGCGGTGTCTCAGCCTGGAGGTCTCTGAGACTCTCC 540  
 Db 481 GTGCACTGTGAGATCTGGGAGGCGGTGTCTCAGCCTGGAGGTCTCTGAGACTCTCC 540  
 Qy 541 TGTGCAAGCTCTGAGATTCCTCTTCAAGACTTGTCTAATGCACTGGGTCCGAGGCTCTA 600  
 Db 541 TGTGCAAGCTCTGAGATTCCTCTTCAAGACTTGTCTAATGCACTGGGTCCGAGGCTCTA 600  
 Qy 601 GCGAAGGAGGCTGAGATGGGAGTGGCACTTATCATATGATGAGAGCACTAAATACATACGA 660  
 Db 601 GCGAAGGAGGCTGAGATGGGAGTGGCACTTATCATATGATGAGAGCACTAAATACATACGA 660  
 Qy 661 GACTCCGTAAGGCGCATTCATCCATCTCCAGAGACCTTCCAGAGACCGGTGTATCTA 720  
 Db 661 GACTCCGTAAGGCGCATTCATCCATCTCCAGAGACCTTCCAGAGACCGGTGTATCTA 720  
 Qy 721 AAAATGAACAGCTGAGAACTGAGACACGCGTGTCTATTACTGTGCAAGATCAGAGC 780  
 Db 721 AAAATGAACAGCTGAGAACTGAGACACGCGTGTCTATTACTGTGCAAGATCAGAGC 780  
 Qy 781 CTGTTGGGTGATGATGACCACTACTACGTTTGGAGCTGTGGGCAAAAGGACCAAGTTC 840  
 Db 781 CTGTTGGGTGATGATGACCACTACTACGTTTGGAGCTGTGGGCAAAAGGACCAAGTTC 840  
 Qy 841 ACCGTCCTCTCAGATCCGAAACAAAACCTGATCAGGAGAGATTTGAAACCATCAACAT 900  
 Db 841 ACCGTCCTCTCAGATCCGAAACAAAACCTGATCAGGAGAGATTTGAAACCATCAACAT 900  
 Qy 901 CACCATTAAGTAAGCTT 918  
 Db 901 CACCATTAAGTAAGCTT 918

## RESULT 3 US-09-697-561A-13

; Sequence 13, Application US/09697561A

; GENERAL INFORMATION:

; APPLICANT: Viventia Biotech Inc.

; APPLICANT: Dan, Michael D.  
 ; Maiti, Pradip K.

; APPLICANT: Kaplan, Howard A.

; TITLE OF INVENTION: Antigen Binding Fragments that Specifically Detect Cancer Cells,  
 ; Nucleotides Encoding the fragments....



Db 1 GAATTCATGAAAAAACCGCTATCGGAGATCGAGTTGCACTGCGTGGTTCCGTACCGCTT 60  
Qy 61 GCGCAGCCGATATTTGTTGAGCAGTCTCAGAGCACTCTTGTGTTCCAGGGGAA 120  
Db 61 GCGCAGCCGATATTTGTTGAGCAGTCTCAGAGCACTCTTGTGTTCCAGGGGAA 120  
Qy 121 AGAGCCACCTCTCTGCGAGGGCCAGTCAAGTGTGTTAGTAGCAGTACTTACCTGGTAC 180  
Db 121 AGAGCCACCTCTCTGCGAGGGCCAGTCAAGTGTGTTAGTAGCAGTACTTACCTGGTAC 180  
Qy 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTCATCTCCAGGGCCACT 240  
Db 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTCATCTCCAGGGCCACT 240  
Qy 241 GCGATCCAGACAGTTTCACTGAGTGGGTCGCGGACAGACTTCACTCTCACTACAGT 300  
Db 241 GCGATCCAGACAGTTTCACTGAGTGGGTCGCGGACAGACTTCACTCTCACTACAGT 300  
Qy 301 AGACTGAGCCTGAAAGATTTTGAGTGTATTAATCTGACAGATGATGGTACCTCAG 360  
Db 301 AGACTGAGCCTGAAAGATTTTGAGTGTATTAATCTGACAGATGATGGTACCTCAG 360  
Qy 361 ACACCTCAGATCACTTTCCGCGGAGGACCAAGTGTGATCAAAAGAACTGTGCTGCA 420  
Db 361 ACACCTCAGATCACTTTCCGCGGAGGACCAAGTGTGATCAAAAGAACTGTGCTGCA 420  
Qy 421 CCATCTGTCTCTGCGGAGGCTCCGAGTGTGATGATGATGATGATGATGATGATGAT 480  
Db 421 CCATCTGTCTCTGCGGAGGCTCCGAGTGTGATGATGATGATGATGATGATGATGAT 480  
Qy 481 GTGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
Db 481 GTGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
Qy 541 TGTGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
Db 541 TGTGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
Qy 601 GCGCAGCCGATATTTGTTGAGCAGTCTCAGAGCACTCTTGTGTTCCAGGGGAA 120  
Db 601 GCGCAGCCGATATTTGTTGAGCAGTCTCAGAGCACTCTTGTGTTCCAGGGGAA 120  
Qy 661 GACTCGGTGAGGCGGATTTACCATCTCCAGAGCACTTCCAGAGCACTGATCTCA 720  
Db 661 GACTCGGTGAGGCGGATTTACCATCTCCAGAGCACTTCCAGAGCACTGATCTCA 720  
Qy 721 AAAATGACAGCTGAGAACTGAGACAGGCTGTCTATTAATCTGTGAGAGATCAAGAGC 780  
Db 721 AAAATGACAGCTGAGAACTGAGACAGGCTGTCTATTAATCTGTGAGAGATCAAGAGC 780  
Qy 781 CTGTTGGGTGACTATGACCACTACGTTTGGAGGTGCGGGCAAGGGGACCAAGGTC 840  
Db 781 CTGTTGGGTGACTATGACCACTACGTTTGGAGGTGCGGGCAAGGGGACCAAGGTC 840  
Qy 841 ACCGTCCTCTCAGATCCGAAACAAAATGATCAGGAGAGAGATGATCACTCACT 900  
Db 841 ACCGTCCTCTCAGATCCGAAACAAAATGATCAGGAGAGAGATGATCACTCACT 900  
Qy 901 CACCATTAAGTGAAGCTT 918  
Db 901 CACCATTAAGTGAAGCTT 918

RESULT 5  
US-09-782-397A-13

Sequence 13, Application US/09782397A

GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

Mailli, Pradip K.

Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND

DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397A  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/862,124  
FILING DATE: 22-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 918 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1..906, 913..918)  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-782-397A-13

Query Match 100.0%; Score 918; DB 33; Length 918;  
Best Local Similarity 100.0%; Pred. No. 2.5e-225;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAATTCATGAAAAAACCGCTATCGGAGATCGAGTTGCACTGCGTGGTTCCGTACCGCTT 60  
Db 1 GAATTCATGAAAAAACCGCTATCGGAGATCGAGTTGCACTGCGTGGTTCCGTACCGCTT 60  
Qy 61 GCGCAGCCGATATTTGTTGAGCAGTCTCAGAGCACTCTTGTGTTCCAGGGGAA 120  
Db 61 GCGCAGCCGATATTTGTTGAGCAGTCTCAGAGCACTCTTGTGTTCCAGGGGAA 120  
Qy 121 AGAGCCACCTCTCTGCGAGGGCCAGTCAAGTGTGTTAGTAGCAGTACTTACCTGGTAC 180  
Db 121 AGAGCCACCTCTCTGCGAGGGCCAGTCAAGTGTGTTAGTAGCAGTACTTACCTGGTAC 180  
Qy 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTCATCTCCAGGGCCACT 240  
Db 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTCATCTCCAGGGCCACT 240  
Qy 241 GCGATCCAGACAGTTTCACTGAGTGGGTCGCGGACAGACTTCACTCTCACTACAGT 300  
Db 241 GCGATCCAGACAGTTTCACTGAGTGGGTCGCGGACAGACTTCACTCTCACTACAGT 300  
Qy 301 AGACTGAGCCTGAAAGATTTTGAGTGTATTAATCTGACAGATGATGGTACCTCAG 360  
Db 301 AGACTGAGCCTGAAAGATTTTGAGTGTATTAATCTGACAGATGATGGTACCTCAG 360  
Qy 361 ACACCTCAGATCACTTTCCGCGGAGGACCAAGTGTGATCAAAAGAACTGTGCTGCA 420  
Db 361 ACACCTCAGATCACTTTCCGCGGAGGACCAAGTGTGATCAAAAGAACTGTGCTGCA 420

QY 421 CCATCTGCTCTGAGGCTGAGCGCTTCCGAGAGTGTGATCATGCTGAGTGTGCTCCAG 480  
 DB 421 CCATCTGCTCTGAGGCTGAGCGCTTCCGAGAGTGTGATCATGCTGAGTGTGCTCCAG 480  
 QY 481 GTGACGTGTGTGAGTCTGTGGGAGAGCGTGTCTCAGACCTGGAGAGTCCCTGAGACTGCC 540  
 DB 481 GTGACGTGTGTGAGTCTGTGGGAGAGCGTGTCTCAGACCTGGAGAGTCCCTGAGACTGCC 540  
 QY 541 TGTGACGCTCTGAGTTCCTCCCTTCAAGAGCTTGTCTATGCACTGGGTCCGCAAGCTCTA 600  
 DB 541 TGTGACGCTCTGAGTTCCTCCCTTCAAGAGCTTGTCTATGCACTGGGTCCGCAAGCTCTA 600  
 QY 601 GGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGCACTAAATACCTACGCA 660  
 DB 601 GGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGCACTAAATACCTACGCA 660  
 QY 661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAGAACACCGTGTATCTA 720  
 DB 661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAGAACACCGTGTATCTA 720  
 QY 721 AAAATGAACAGCTGAGAACTGAGAGACAGCGCTGTCTATTACTGTGCGAGATCATAGAC 780  
 DB 721 AAAATGAACAGCTGAGAACTGAGAGACAGCGCTGTCTATTACTGTGCGAGATCATAGAC 780  
 QY 781 CTGTTGGGTGACTATGACCACTACTACGCTTGTGACGCTGTGGGCAAGGAGCACGCTC 840  
 DB 781 CTGTTGGGTGACTATGACCACTACTACGCTTGTGACGCTGTGGGCAAGGAGCACGCTC 840  
 QY 841 ACCGCTCTCTCAGATCCGAACTGAGAGACAGCGCTGTCTATTACTGTGCGAGATCATAGAC 900  
 DB 841 ACCGCTCTCTCAGATCCGAACTGAGAGACAGCGCTGTCTATTACTGTGCGAGATCATAGAC 900  
 QY 901 CACCATTTAGTGAAGCTT 918  
 DB 901 CACCATTTAGTGAAGCTT 918

## RESULT 6

US-09-782-397B-13

Sequence 13, Application US/09782397B

GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

Maity, Pradip K.

Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES

ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison &amp; Foerster LLP

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/782,397B

FILING DATE: 13-Feb-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/862,124

FILING DATE: 1997-05-22

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600  
 TELEFAX: (650) 494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 918 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: join(1..906, 913..918)  
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
 US-09-782-397B-13

Query Match 100.0%; Score 918; DB 33; Length 918;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-225;  
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCCGCTATCGCATCGCATGTCACCTGCTGCTTCCGAGGAA 60  
 DB 1 GAATTCATGAAAAAACCCGCTATCGCATCGCATGTCACCTGCTGCTTCCGAGGAA 60  
 QY 61 GGCGAGGCGGATATGTTGTTGACGAGCTCCAGGACCGCTGCTTGTCTCCAGGAA 120  
 DB 61 GGCGAGGCGGATATGTTGTTGACGAGCTCCAGGACCGCTGCTTGTCTCCAGGAA 120  
 QY 121 AGAGCCACCTCTCTCTGAGAGGCGCATCAGAGTGTATGAGCACTTACTTAACTGCTGATC 180  
 DB 121 AGAGCCACCTCTCTCTGAGAGGCGCATCAGAGTGTATGAGCACTTACTTAACTGCTGATC 180  
 QY 181 CAGCAGAACTGTGGCCAGGCTCCAGGCTCTCATTTATGTGATCATCCAGGCGCACT 240  
 DB 181 CAGCAGAACTGTGGCCAGGCTCCAGGCTCTCATTTATGTGATCATCCAGGCGCACT 240  
 QY 241 GGCGATCCAGACAGTTCAGTGTGAGTGGGTCCGGGACAGACTTCACTCAACCATCAGT 300  
 DB 241 GGCGATCCAGACAGTTCAGTGTGAGTGGGTCCGGGACAGACTTCACTCAACCATCAGT 300  
 QY 301 AGACTGAGCCTGGAAGATTTTGGAGTATTACTGTACAGAGTATGATGATGATGATGATGATGAT 360  
 DB 301 AGACTGAGCCTGGAAGATTTTGGAGTATTACTGTACAGAGTATGATGATGATGATGATGATGAT 360  
 QY 361 ACACCTCAATCACTTTCGCGGAGAGGACCAAGTGTGAATCAAGAACTGTGTGTGA 420  
 DB 361 ACACCTCAATCACTTTCGCGGAGAGGACCAAGTGTGAATCAAGAACTGTGTGTGA 420  
 QY 421 CCATCTGCTCTGAGCGGTGCGGCTTCCGAGGTGTGATCAGTGTGAGTGTGCTCCAG 480  
 DB 421 CCATCTGCTCTGAGCGGTGCGGCTTCCGAGGTGTGATCAGTGTGAGTGTGCTCCAG 480  
 QY 481 GTGACAGCTGTGAGAGTCTGTGGGAGAGCGTGTCTCAGACCTGGAGAGTCCCTGAGACTGCC 540  
 DB 481 GTGACAGCTGTGAGAGTCTGTGGGAGAGCGTGTCTCAGACCTGGAGAGTCCCTGAGACTGCC 540  
 QY 541 TGTGACGCTCTGAGTTCCTCCCTTCAAGAGCTTGTCTATGCACTGGGTCCGCAAGCTCTA 600  
 DB 541 TGTGACGCTCTGAGTTCCTCCCTTCAAGAGCTTGTCTATGCACTGGGTCCGCAAGCTCTA 600  
 QY 601 GGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGCACTAAATACCTACGCA 660  
 DB 601 GGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGCACTAAATACCTACGCA 660  
 QY 661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAGAACACCGTGTATCTA 720  
 DB 661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAGAACACCGTGTATCTA 720  
 QY 721 AAAATGAACAGCTGAGAACTGAGAGACAGCGCTGTCTATTACTGTGCGAGATCATAGAC 780  
 DB 721 AAAATGAACAGCTGAGAACTGAGAGACAGCGCTGTCTATTACTGTGCGAGATCATAGAC 780  
 QY 781 CTGTTGGGTGACTATGACCACTACTACGCTTGTGACGCTGTGGGCAAGGAGCACGCTC 840  
 DB 781 CTGTTGGGTGACTATGACCACTACTACGCTTGTGACGCTGTGGGCAAGGAGCACGCTC 840







241 GGCATGCGCAGACAGGTTCAGTGGCAGTGGGTCCGGGACAGACTTCACTCCACATCACT 300  
Db 678 GGCATGCGCAGACAGGTTCAGTGGCAGTGGGTCCGGGACAGACTTCACTCCACATCACT 619  
Qy 301 AGACTGGAACCTGAAGATTTTGCAGTGTAATTACTGCAGCAGTATGGTAGCTCACTCAG 360  
Db 618 AGACTGGAACCTGAAGATTTTGCAGTGTAATTACTGCAGCAGTATGGTAGCTCACTCAG 559  
Qy 361 ACACCTCAGATCACTTTCCGCGGAGGGACCAAGSTGAGATCAACGAACTGTGGCTGCA 420  
Db 558 ACACCTCAGATCACTTTCCGCGGAGGGACCAAGSTGAGATCAACGAACTGTGGCTGCA 499  
Qy 421 CCATCTGTCTCTGCGCGGTGGCGGTTCCGAGAGGTGTGGATCAGGTGAGGTGGCTCCAG 480  
Db 498 CCATCTGTCTCTGCGCGGTGGCGGTTCCGAGAGGTGTGGATCAGGTGAGGTGGCTCCAG 439  
Qy 481 GTCGACGCTGTGAGAGTCTGGGGGAGGGCGGTCTCACCTGGGAGGTCCCTGAAACTCTCC 540  
Db 438 GTGACGCTGTGTGAAGTCTGGGGGAGGGCGGTGTCAAGCTGGGAGGTCCCTGAAACTCTCC 379  
Qy 541 TGTGCAAGCTCTGGAATCCCTTCAGAAAGCTTGTCTATGCACTGGGTCCGCGAGCTCTA 600  
Db 378 TGTGCAAGCTCTGGAATCCCTTCAGAAAGCTTGTCTATGCACTGGGTCCGCGAGCTCTA 319  
Qy 601 GGCAAGGGGCTGAGTGGGTGGCGAGTTATATCATATGATGGAAGCACTAAATACAGCA 660  
Db 318 GGCAAGGGGCTGAGTGGGTGGCGAGTTATATCATATGATGGAAGCACTAAATACAGCA 259  
Qy 661 GACTCCGTGGAAGGGCGCATTCACATCTCCAGAGACACTTCCAAAGAACACGGGTGATCTA 720  
Db 258 GACTCCGTGGAAGGGCGCATTCACATCTCCAGAGACACTTCCAAAGAACACGGGTGATCTA 199  
Qy 721 AAAATGAACAGCGCTGAGACTGAGGACAGGGCGTCTATTACTGTCGCGAGATCGAGAGC 780  
Db 198 AAAATGAACAGCGCTGAGACTGAGGACAGGGCGTCTATTACTGTCGCGAGATCGAGAGC 139  
Qy 781 CTGTTGGGTGAATATGACCACTACTACGGTTTGGACGTCGTGGGCGAAAGGACCAAGGTC 840  
Db 138 CTGTTGGGTGAATATGACCACTACTACGGTTTGGACGTCGTGGGCGAAAGGACCAAGGTC 79  
Qy 841 ACCGTCCTCTCAGATCCGAAACAAAACCTGATCAGGAAAGAAAGATTTGAACCATCAACAT 900  
Db 78 ACCGTCCTCTCAGATCCGAAACAAAACCTGATCAGGAAAGAAAGATTTGAACCATCAACAT 19  
Qy 901 CACCATTAAGTGAAGCTT 918  
Db 18 CACCATTAAGTGAAGCTT 1

```

RESULT 10
US-09-697-561A-15/c
; Sequence 15, Application US/09697561A
; GENERAL INFORMATION:
; APPLICANT: Viventia Biotech Inc.
; APPLICANT: Dan, Michael D
; APPLICANT: Malti, Pradip K
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: Antigen Binding Fragments that Specifically Detect Cancer Cells,
; TITLE OF INVENTION: Nucleotides Encoding the fragments...
; FILE REFERENCE: 830001-2001.1
; CURRENT APPLICATION NUMBER: US/09/697,561A
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 08/862,124
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-09-697-561A-15

```

Query Match Similarity		99.8%	Score 916.4	DB 30	Length 918
Best Local Similarity		99.9%	Pred. No. 6	5e-225	
Matches	917	Conservative	0	Mismatches	1
				Indels	0
				Gaps	0
QY	1	GAATTCATGAAAAA	CCGCTATCGCGATCGCAGTTGCACTGCGTTCGTTACCGTT	60	
DB	918	GAATTCATGAAAAA	ACCGCTATCGCGATCGCAGTTGCACTGCGTTCGTTACCGTT	859	
QY	61	GCGCAGGCGCAT	TATGTGTTGACGCAAGTCCTCAGGCAACCTGTCTTTGTCTCAGGGGAA	120	
DB	858	GCGCAGGCGCAT	TATGTGTTGACGCAAGTCCTCAGGCAACCTGTCTTTGTCTCAGGGGAA	799	
QY	121	AGAGCCACCCCTCT	CCCTGCAAGGCGCAGTCAGAGTGTATGAGAGCACTTAGCCTGATAC	180	
DB	798	AGAGCCACCCCTCT	CCCTGCAAGGCGCAGTCAGAGTGTATGAGAGCACTTAGCCTGATAC	739	
QY	181	CAGCAAAAACCTG	GCAGGCTCCAGGCTCTCATCTATAGTGATCCACAGGGGCAC	240	
DB	728	CAGCAAAAACCTG	GCAGGCTCCAGGCTCTCATCTATAGTGATCCACAGGGGCAC	679	
QY	241	GGCATTCGACAG	CAAGTTCAATGAGCAGTGGTCCGGGACAGACTTCACTTACATCAAT	300	
DB	678	GGCATTCGACAG	CAAGTTCAATGAGCAGTGGTCCGGGACAGACTTCACTTACATCAAT	619	
QY	301	AGACTGAGCCTG	AAGATTTTTCGACATGTATTAATCTGTCAGCAGATATGATGTCACCTCAG	360	
DB	618	AGACTGAGCCTG	AAGATTTTTCGACATGTATTAATCTGTCAGCAGATATGATGTCACCTCAG	559	
QY	361	AACCTTCAGATCA	CTTTTCGCGCGAGGAGCAAGAGTGAGATCAAAAGAACTGTGCTGCA	420	
DB	558	AACCTTCAGATCA	CTTTTCGCGCGAGGAGCAAGAGTGAGATCAAAAGAACTGTGCTGCA	499	
QY	421	CCATCTGTCTCT	GTGGGGTGGCGGTTCCGGAGGTGGTGGATCAAGTGTGAGGTGGCTCCAG	480	
DB	498	CCATCTGTCTCT	GTGGGGTGGCGGTTCCGGAGGTGGTGGATCAAGTGTGAGGTGGCTCCAG	439	
QY	481	GTGCAGCTGTG	AGTCTGCGGAGGCGGTGTCACAGCTGGAGAGGTCCCTGAGACTCTCC	540	
DB	438	GTGCAGCTGTG	AGTCTGCGGAGGCGGTGTCACAGCTGGAGAGGTCCCTGAGACTCTCC	379	
QY	541	TGTGACGCTCT	GTGATTCCTCCCTTCAGAACTTTTGCTATGCACTGAGTCCGCAAGCTCTA	600	
DB	378	TGTGACGCTCT	GTGATTCCTCCCTTCAGAACTTTTGCTATGCACTGAGTCCGCAAGCTCTA	319	
QY	601	GGCAAGGGGCTG	AGTGGGTGGCGATTATATCATATGATGGAAGCACTAAATATCATACGCA	660	
DB	318	GGCAAGGGGCTG	AGTGGGTGGCGATTATATCATATGATGGAAGCACTAAATATCATACGCA	259	
QY	661	GACTCCGTGAA	AGGGCCGATTCACCATCTCCAGAGACACTTCCAAAGAACAGCGTGTATCTA	720	
DB	258	GACTCCGTGAA	AGGGCCGATTCACCATCTCCAGAGACACTTCCAAAGAACAGCGTGTATCTA	199	
QY	721	AAAAATGAAC	AGCTGTAGACCTGAGGACACGCGTGTCTATTAATCTGTGCGAGATCAGAC	780	
DB	198	AAAAATGAAC	AGCTGTAGACCTGAGGACACGCGTGTCTATTAATCTGTGCGAGATCAGAC	139	
QY	781	CTGTTTGGGTG	ACTATGACACTTACCGTTTGGACGTCTGGGGCAAAAGGACCAACGGTC	840	
DB	138	CTGTTTGGGTG	ACTATGACACTTACCGTTTGGACGTCTGGGGCAAAAGGACCAACGGTC	79	
QY	841	ACCGTCTCTCA	GAGTCCGGAACAAAAAATGATCAGCGAAGAAAGATCTGAACATCAACAT	900	
DB	78	ACCGTCTCTCA	GAGTCCGGAACAAAAAATGATCAGCGAAGAAAGATCTGAACATCAACAT	19	
QY	901	CACCATTAATG	ATAAGCTT 918		
DB	18	CACCATTAATG	ATAAGCTT 1		

RESULT 11  
US-09-782-397-15/c  
; Sequence 15, Application US/09782397  
; GENERAL INFORMATION:

APPLICANT: Dan, Michael D.  
Maltz, Pradip K.  
Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 918 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-782-387-15  
Query Match 99.8%; Score 916.4; DB 33; Length 918;  
Best Local Similarity 99.9%; Pred. No. 6.5e-225;  
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GAATTCATGAAAAACCGCTATCGCATCGCATGTCAGTGGCTGTTGCTACCGTT 60  
918 GAATTCATGAAAAACCGCTATCGCATCGCATGTCAGTGGCTGTTGCTACCGTT 859  
61 GCGCAGGCGCATATGTTGTTGACGAGTCTCCAGGACCTGTTTGTCTCCAGGGAA 120  
858 GCGCAGGCGCATATGTTGTTGACGAGTCTCCAGGACCTGTTTGTCTCCAGGGAA 799  
121 AAGGCCACCTCTCTCTGCGAGGCGCATGAGTGTAGAGAGCTACTTGGCTGTAC 180  
798 AAGGCCACCTCTCTCTGCGAGGCGCATGAGTGTAGAGAGCTACTTGGCTGTAC 739  
181 CAGCAGAACTGGCCAGGCTCCAGGCTCTCATCTATGATGATCCAGAGGCACT 240  
738 CAGCAGAACTGGCCAGGCTCCAGGCTCTCATCTATGATGATCCAGAGGCACT 679  
241 GCGATGCCAGACAGGTTCAAGTGGCACTGGGTCGCGGACAGACTTCACTTCACT 300  
678 GCGATGCCAGACAGGTTCAAGTGGCACTGGGTCGCGGACAGACTTCACTTCACT 619  
301 AAGCTGAGCTGGAATTTGAGTGTATTAATCTGACAGATGATGATGATGATGAT 360  
618 AAGCTGAGCTGGAATTTGAGTGTATTAATCTGACAGATGATGATGATGATGAT 559  
361 ACACCTCAATCACTTTCGCGGAGGAGCCAAAGTGGAGATCAAAAGAACTGTGCTGCA 420

558 ACACCTCAATCACTTTCGCGGAGGAGCCAAAGTGGAGATCAAAAGAACTGTGCTGCA 499  
421 CCATCTGCTCTGCGCGGTGCGGTTCCGAGAGTGTGATGATGATGATGATGATGAT 480  
498 CCATCTGCTCTGCGCGGTGCGGTTCCGAGAGTGTGATGATGATGATGATGATGAT 439  
481 GTGAGAGCTGTGAGTGTGAGGAGGCGTGTCCAGGCTGGAGAGTCCCTGAGACTCC 540  
438 GTGAGAGCTGTGAGTGTGAGGAGGCGTGTCCAGGCTGGAGAGTCCCTGAGACTCC 379  
541 TGTGAGAGCTGTGAGTGTGAGGAGGCGTGTCCAGGCTGGAGAGTCCCTGAGACTCC 600  
378 TGTGAGAGCTGTGAGTGTGAGGAGGCGTGTCCAGGCTGGAGAGTCCCTGAGACTCC 319  
601 GCGAAGGCGCTGAGTGTGAGGAGGCGTGTCCAGGCTGGAGAGTCCCTGAGACTCC 660  
318 GCGAAGGCGCTGAGTGTGAGGAGGCGTGTCCAGGCTGGAGAGTCCCTGAGACTCC 259  
661 GACTCCGTAAGAGGCGGATTCACATCTCCAGAGACCTTCCAAAGACAGGCTGATCTA 720  
258 GACTCCGTAAGAGGCGGATTCACATCTCCAGAGACCTTCCAAAGACAGGCTGATCTA 199  
721 AAATGAACAGCTGAGAACTGAGACACGCTGTCTATTAATCTGCGAGATGAGAGC 780  
198 AAATGAACAGCTGAGAACTGAGACACGCTGTCTATTAATCTGCGAGATGAGAGC 139  
781 CTTGTTGGGATATGACCACTACTACGTTTGAAGTCTGGGCGAAGAGGACACGCTC 840  
138 CTTGTTGGGATATGACCACTACTACGTTTGAAGTCTGGGCGAAGAGGACACGCTC 79  
841 ACCGTCCTCTCAGATTCGAGCAAAAAGTATGATGAGAGAAAGATCTGAACATCACT 900  
78 ACCGTCCTCTCAGATTCGAGCAAAAAGTATGATGAGAGAAAGATCTGAACATCACT 19  
901 CACCATTAAGTGAAGCTT 918  
18 CACCATTAAGTGAAGCTT 1

RESULT 12  
US-09-782-397A-15/C  
Sequence 15, Application US/09782397A  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
Maltz, Pradip K.  
Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397A  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/862,124  
FILING DATE: 22-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnardt, Susan K.

REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 918 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-782-397A-15

Query Match 99.8%; Score 916.4; DB 33; Length 918;  
Best Local Similarity 99.9%; Pred. No. 6.5e-225;  
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GAATTCATGAAAAAACCCTATCGGATCGAGTTCAGTGGCTGGTTCCTACCGT 60  
918 GAATTCATGAAAAAACCCTATCGGATCGAGTTCAGTGGCTGGTTCCTACCGT 859

61 GGGCAGCCGATATTGTGTGAGCGAGTCTCCAGGCACTCTTCTTTCTCCAGGGGAA 120  
858 GGGCAGCCGATATTGTGTGAGCGAGTCTCCAGGCACTCTTCTTTCTCCAGGGGAA 799

121 AGAGCCACCTCTCTGCAAGGGCAGTCAAGAGTGTAGTAGCAGTACTTACCTGTATC 180  
798 AGAGCCACCTCTCTGCAAGGGCAGTCAAGAGTGTAGTAGCAGTACTTACCTGTATC 739

181 CAGCAGAAACCTGGCCAGGCTCCAGAGCTCTCATCATGTATGTGCATCCAGAGGCACT 240  
738 CAGCAGAAACCTGGCCAGGCTCCAGAGCTCTCATCATGTATGTGCATCCAGAGGCACT 679

241 GGCATGCCAGACAGGTTCAAGTGGTCCGGGACAGACTTCACTCTCACCATCACT 300  
678 GGCATGCCAGACAGGTTCAAGTGGTCCGGGACAGACTTCACTCTCACCATCACT 619

301 AGACTGGAAGCTGAAGATTTTGAGTGTATTAAGTCAAGAGTGTATGATGATCACTCCAG 360  
618 AGACTGGAAGCTGAAGATTTTGAGTGTATTAAGTCAAGAGTGTATGATGATCACTCCAG 559

361 ACACCTCAGATCACTTTCGGCGAGGAGCAAGTGAAGTCAAGCACTGTGGCTGCA 420  
558 ACACCTCAGATCACTTTCGGCGAGGAGCAAGTGAAGTCAAGCACTGTGGCTGCA 499

421 CCATCTGTCTTGGCGGCTGGCTTCGGAAGTGTGATCAGTGAAGGCTGCCAG 480  
498 CCATCTGTCTTGGCGGCTGGCTTCGGAAGTGTGATCAGTGAAGGCTGCCAG 439

481 GTGCAAGCTGTGAGTCTGGGAGGAGGCTGTCACCTGGAGGCTCCAGACTCTCC 540  
438 GTGCAAGCTGTGAGTCTGGGAGGAGGCTGTCACCTGGAGGCTCCAGACTCTCC 379

541 TGTGCAAGCTGTGATTTCCCTTCAGAACTTGTCTATCAGTGGTCCGAGGCTCTA 600  
378 TGTGCAAGCTGTGATTTCCCTTCAGAACTTGTCTATCAGTGGTCCGAGGCTCTA 319

601 GGCAGAGGCTGAGTGGTGGGAGGCTTATATCATATGATGAAGCACTAATATCTACGA 660  
318 GGCAGAGGCTGAGTGGTGGGAGGCTTATATCATATGATGAAGCACTAATATCTACGA 259

661 GACTCCGTAAGGGCCGATTCACCATCTCCAGAGACCTTCCAGAAACCGGCTATCTA 720  
258 GACTCCGTAAGGGCCGATTCACCATCTCCAGAGACCTTCCAGAAACCGGCTATCTA 199

721 AAAATGAAGCCTGAGAACTGAGACAGGCTGTCTATATCTGTGAGAGATCAGAGC 780  
198 AAAATGAAGCCTGAGAACTGAGACAGGCTGTCTATATCTGTGAGAGATCAGAGC 139

781 CTGTTGGTGAATGACCACTACGAGTGTGAGAGTGTGGGCAAGGAGCAACGCTC 840

Db 138 CTGTTGGTGAATGACCACTACGAGTGTGAGAGTGTGGGCAAGGAGCAACGCTC 79  
Qy 841 ACCGTCCTCCAGATCCGACAAAAAATGATCAGGAGAAAGATCTGAACCATCACT 900  
Db 78 ACCGTCCTCCAGATCCGACAAAAAATGATCAGGAGAAAGATCTGAACCATCACT 19

Qy 901 CACCATTAAGTGAAGCTT 918  
Db 18 CACCATTAAGTGAAGCTT 1

## RESULT 13

US-09-782-397B-15/C  
Sequence 15, Application US/09782397B  
GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

Mafti, Pradip K.

Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster LLP

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/782,397B

FILING DATE: 13-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/862,124

FILING DATE: 1997-05-22

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141

SEQUENCE CHARACTERISTICS:

LENGTH: 918 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-782-397B-15

Query Match 99.8%; Score 916.4; DB 33; Length 918;  
Best Local Similarity 99.9%; Pred. No. 6.5e-225;  
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GAATTCATGAAAAAACCCTATCGGATCGAGTTCAGTGGCTGGTTCCTACCGT 60  
918 GAATTCATGAAAAAACCCTATCGGATCGAGTTCAGTGGCTGGTTCCTACCGT 859

61 GGCAGCCGATATTGTGTGAGCGAGTCTCCAGGCACTCTTCTTTCTCCAGGGGAA 120  
858 GGCAGCCGATATTGTGTGAGCGAGTCTCCAGGCACTCTTCTTTCTCCAGGGGAA 799

121 AGAGCCACCTCTCTGCAAGGGCAGTCAAGAGTGTAGTAGCAGTACTTACCTGTATC 180

```

Db      798 AGAGGACCCCTCTCTGCGAGGGCCAGTACAGTGTAGTACAGTACTTACGCTGGTAC 739
Qy      181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCTATCTATGTGATCCACAGGCTACT 240
Db      738 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCTATCTATGTGATCCACAGGCTACT 679
Qy      241 GGCATGCGACAGAGGTTCAGTGGGAGTGGGTCGGGACAGACTTCACTTCACTCAGT 300
Db      678 GGCATGCGACAGAGGTTCAGTGGGAGTGGGTCGGGACAGACTTCACTTCACTCAGT 619
Qy      301 AGACTGAGGCTGAGATTTTTCAGTGTATTTACTGTGAGATGATGATGATGATGATGAT 360
Db      618 AGACTGAGGCTGAGATTTTTCAGTGTATTTACTGTGAGATGATGATGATGATGATGAT 559
Qy      361 ACACCTGAGTCACTTTTCGGGAGGAGGACCAAGTGGAGATCAAAACCAACTGTGGCTGCA 420
Db      558 ACACCTGAGTCACTTTTCGGGAGGAGGACCAAGTGGAGATCAAAACCAACTGTGGCTGCA 499
Qy      421 CCATCTGCTCTGGGAGGAGGCTTCCGAGAGTGGTGGATCAGGTTGAGGCTGCTCCAG 480
Db      498 CCATCTGCTCTGGGAGGAGGCTTCCGAGAGTGGTGGATCAGGTTGAGGCTGCTCCAG 439
Qy      481 GTGACGCTGTGAGTCTGGGAGGAGGCTGTGCTCAGGCTGGAGGCTCCTGAGACTCTCC 540
Db      438 GTGACGCTGTGAGTCTGGGAGGAGGCTGTGCTCAGGCTGGAGGCTCCTGAGACTCTCC 379
Qy      541 TGTGACGCTGTGAGTCTGGGAGGAGGCTGTGCTCAGGCTGGAGGCTCCTGAGACTCTCC 600
Db      378 TGTGACGCTGTGAGTCTGGGAGGAGGCTGTGCTCAGGCTGGAGGCTCCTGAGACTCTCC 319
Qy      601 GGCAGAGGAGGCTGAGTGGGAGGAGGCTGATATATATATATATATATATATATATATAT 660
Db      318 GGCAGAGGAGGCTGAGTGGGAGGAGGCTGATATATATATATATATATATATATATATAT 259
Qy      661 GACTCCGTGAGAGGAGGCTGAGTGGGAGGAGGCTGATATATATATATATATATATATAT 720
Db      258 GACTCCGTGAGAGGAGGCTGAGTGGGAGGAGGCTGATATATATATATATATATATATAT 199
Qy      721 AAAATGAAACAGCTGAGAACTGAGAGACAGGCTGTCTATTTACTGTGAGAGATCAAGC 780
Db      198 AAAATGAAACAGCTGAGAACTGAGAGACAGGCTGTCTATTTACTGTGAGAGATCAAGC 139
Qy      781 CTGTTGGGTACTATGACCTACTACTACGTTTGGACGCTGGGGCAAAAGGAGCCAGGCT 840
Db      138 CTGTTGGGTACTATGACCTACTACTACGTTTGGACGCTGGGGCAAAAGGAGCCAGGCT 79
Qy      841 ACCGCTCTCTCAGATCCGAACAAAAAGTATCAGCGAAGAGATCTGAACCATCAGAT 900
Db      78 ACCGCTCTCTCAGATCCGAACAAAAAGTATCAGCGAAGAGATCTGAACCATCAGAT 19
Qy      901 CACCATTAAGTGAAGCTT 918
Db      18 CACCATTAAGTGAAGCTT 1

```

```

; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-09-782-397C-15

Query Match      99.8%; Score 916.4; DB 33; Length 918;
Best Local Similarity 99.9%; Pred. No. 6.5e-225;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAATTCATGAAAAAACCCTATTCGATGCGATGCGATGCGATGCGATGCGATGCGATGCGAT 60
Db      918 GAATTCATGAAAAAACCCTATTCGATGCGATGCGATGCGATGCGATGCGATGCGATGCGAT 859
Qy      61 GCGCAGGCGGATATGTTGTTGAGCGAGTCCAGGACCTGCTTGTCTCCAGGGGAA 120
Db      858 GCGCAGGCGGATATGTTGTTGAGCGAGTCCAGGACCTGCTTGTCTCTCCAGGGGAA 799
Qy      121 AGAGCACCCTCTCTGAGGAGGCTCAGAGTGTATGAGCAGTACTTATGCTGTAGC 180
Db      798 AGAGCACCCTCTCTGAGGAGGCTCAGAGTGTATGAGCAGTACTTATGCTGTAGC 739
Qy      181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCTATCTATGTGATCCACAGGCTACT 240
Db      738 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCTATCTATGTGATCCACAGGCTACT 679
Qy      241 GGCATGCGACAGAGGTTCAGTGGGAGTGGGTCGGGACAGACTTCACTTCACTCAGT 300
Db      678 GGCATGCGACAGAGGTTCAGTGGGAGTGGGTCGGGACAGACTTCACTTCACTCAGT 619
Qy      301 AGACTGAGGCTGAGATTTTTCAGTGTATTTACTGTGAGATGATGATGATGATGATGAT 360
Db      618 AGACTGAGGCTGAGATTTTTCAGTGTATTTACTGTGAGATGATGATGATGATGATGAT 559
Qy      361 ACACCTGAGTCACTTTTCGGGAGGAGGACCAAGTGGAGATCAAAACCAACTGTGGCTGCA 420
Db      558 ACACCTGAGTCACTTTTCGGGAGGAGGACCAAGTGGAGATCAAAACCAACTGTGGCTGCA 499
Qy      421 CCATCTGCTCTGGGAGGAGGCTTCCGAGAGTGGTGGATCAGGTTGAGGCTGCTCCAG 480
Db      498 CCATCTGCTCTGGGAGGAGGCTTCCGAGAGTGGTGGATCAGGTTGAGGCTGCTCCAG 439
Qy      481 GTGACGCTGTGAGTCTGGGAGGAGGCTGTGCTCAGGCTGGAGGCTCCTGAGACTCTCC 540
Db      438 GTGACGCTGTGAGTCTGGGAGGAGGCTGTGCTCAGGCTGGAGGCTCCTGAGACTCTCC 379
Qy      541 TGTGACGCTGTGAGTCTGGGAGGAGGCTGTGCTCAGGCTGGAGGCTCCTGAGACTCTCC 600
Db      378 TGTGACGCTGTGAGTCTGGGAGGAGGCTGTGCTCAGGCTGGAGGCTCCTGAGACTCTCC 319
Qy      601 GGCAGAGGAGGCTGAGTGGGAGGAGGCTGATATATATATATATATATATATATATATAT 660
Db      318 GGCAGAGGAGGCTGAGTGGGAGGAGGCTGATATATATATATATATATATATATATATAT 259
Qy      661 GACTCCGTGAGAGGAGGCTGAGTGGGAGGAGGCTGATATATATATATATATATATATAT 720
Db      258 GACTCCGTGAGAGGAGGCTGAGTGGGAGGAGGCTGATATATATATATATATATATATAT 199
Qy      721 AAAATGAAACAGCTGAGAACTGAGAGACAGGCTGTCTATTTACTGTGAGAGATCAAGC 780
Db      198 AAAATGAAACAGCTGAGAACTGAGAGACAGGCTGTCTATTTACTGTGAGAGATCAAGC 139
Qy      781 CTGTTGGGTACTATGACCTACTACTACGTTTGGACGCTGGGGCAAAAGGAGCCAGGCT 840
Db      138 CTGTTGGGTACTATGACCTACTACTACGTTTGGACGCTGGGGCAAAAGGAGCCAGGCT 79
Qy      841 ACCGCTCTCTCAGATCCGAACAAAAAGTATCAGCGAAGAGATCTGAACCATCAGAT 900
Db      78 ACCGCTCTCTCAGATCCGAACAAAAAGTATCAGCGAAGAGATCTGAACCATCAGAT 19
Qy      901 CACCATTAAGTGAAGCTT 918

```

Db 18 CACCATTAAGTGAAGCTT 1

RESULT 15  
US-08-657-449-16  
Sequence 16, Application US/08657449  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
APPLICANT: Malt, Pradip K.  
APPLICANT: Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT  
SPECIFICALLY DETECT CANCER CELLS  
TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
TREATMENT OF CANCERS  
TITLE OF INVENTION: DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/657,449  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Leinhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.00  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 867 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1..855, 862..867)  
US-08-657-449-16

Query Match 87.1%; Score 799.6; DB 11; Length 867;  
Best Local Similarity 94.0%; Pred. No. 7.4e-195;  
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

QY 1 GAATTCATGAAAAAACCCTATCGCATGCGAGTTGCACTGGCTGGTTCGCTACCGTT 60  
DB 1 GAATTCATGAAAAAACCCTATCGCATGCGAGTTGCACTGGCTGGTTCGCTACCGTT 60  
QY 61 GGGCAGCGCGATTTTGTGTGAGCGAGTCTCCAGGCACTGCTTTGTCTCCAGGGGAA 120  
DB 61 GGGCAGCGCGATTTTGTGTGAGCGAGTCTCCAGGCACTGCTTTGTCTCCAGGGGAA 120  
QY 121 AGAGCACCCTCTCTGCGAGGCGCAGTCAAGAGTTAGTACAGCTACTAGCTGCTG 180  
DB 121 AGAGCACCCTCTCTGCGAGGCGCAGTCAAGAGTTAGTACAGCTACTAGCTGCTG 180  
QY 181 CAGCAGAAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTCATCAACAGGCGCACT 240  
DB 181 CAGCAGAAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTCATCAACAGGCGCACT 240  
QY 241 GGCATGCCAGACAGGTTCACTGTCAGTGGTCCGGGACAGACTTCACTCACTACATCACT 300  
DB 241 GGCATGCCAGACAGGTTCACTGTCAGTGGTCCGGGACAGACTTCACTCACTACATCACT 300

QY 301 AGACTGAGCCTGGAAGATTTTGCAGTGTATTAATCTGTACAGAGTATGTAAGTCACTCAG 360  
DB 301 AGACTGAGCCTGGAAGATTTTGCAGTGTATTAATCTGTACAGAGTATGTAAGTCACTCAG 360  
QY 361 ACACTTCAGATCACTTTGCGCGGAGGACCAAGGTGAATCAAGAACTGTGCTGCA 420  
DB 361 ACACTTCAGATCACTTTGCGCGGAGGACCAAGGTGAATCAAGAACTGTGCTGCA 420  
QY 421 CCATCTGTCTGCGCGGAGGCTTCCGAGGAGTGTATCAGGTGGAAGTGGCTCCAG 480  
DB 421 TC-----CGAGCAG 429  
QY 481 GTGCACTGTGAGAGTCTGCGGAGGCGTGTCTCACTGAGAGTCCCTGAGACTCTCC 540  
DB 430 GTGCACTGTGAGAGTCTGCGGAGGCGTGTCTCACTGAGAGTCCCTGAGACTCTCC 489  
QY 541 TGTGCACTGTGAGATTTCCCTTCAAGAGCTTTGTATGCACTGGTCCGCGAGCTCTA 600  
DB 490 TGTGCACTGTGAGATTTCCCTTCAAGAGCTTTGTATGCACTGGTCCGCGAGCTCTA 549  
QY 601 GGCAGAGGCGTGGAGTGGGTGGCAGTTATATATATATGAGAACTAAATCTACGCA 660  
DB 550 GGCAGAGGCGTGGAGTGGGTGGCAGTTATATATATATGAGAACTAAATCTACGCA 609  
QY 661 GACTCCGTGAAGGCGCATTTCAACATCTCCAGAGCACTTCCAGAAACAGGCTATCTA 720  
DB 610 GACTCCGTGAAGGCGCATTTCAACATCTCCAGAGCACTTCCAGAAACAGGCTATCTA 669  
QY 721 AAATGAACAGCCTGAGAACTAGAGACAGCGCTGTCTATTAATCTGTGCGAGATCAGAGC 780  
DB 670 AAATGAACAGCCTGAGAACTAGAGACAGCGCTGTCTATTAATCTGTGCGAGATCAGAGC 729  
QY 781 CTGTTGGGAGCTATGACCACTACCTACCTGTTGACGTCTGGGCGAAAGGACACAGGTC 840  
DB 730 CTGTTGGGAGCTATGACCACTACCTACCTGTTGACGTCTGGGCGAAAGGACACAGGTC 789  
QY 841 ACCGTCCTCTCAGATCCGAAACAAAACATGATCAGGAGAGATCTGAACATCAACAT 900  
DB 790 ACCGTCCTCTCAGATCCGAAACAAAACATGATCAGGAGAGATCTGAACATCAACAT 849  
QY 901 CACCATTAAGTGAAGCTT 918  
DB 850 CACCATTAAGTGAAGCTT 867

Search completed: September 17, 2003, 05:12:00  
Job time : 2906 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 03:07:19 ; Search time 277 Seconds  
(without alignments)  
2799.666 Million cell updates/sec

Title: US-08-657-449-13

Perfect score: 918  
Sequence: 1 GAATTCATGMAAAACCGC.....ATCACCATTAGTGAAGCTT 918

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 607968 segs, 422389675 residues

Total number of hits satisfying chosen parameters: 1215936

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/prodata/1/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/prodata/1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/prodata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/prodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/prodata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/prodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	5	US-09-194-164-13 Sequence 13, Appl
2	916.4	99.8	918	5	US-09-194-164-15 Sequence 15, Appl
3	799.6	87.1	867	5	US-09-194-164-16 Sequence 16, Appl
4	798	86.9	867	5	US-09-194-164-18 Sequence 18, Appl
5	457	39.8	1103	1	PCT-US03-14964-4 Sequence 4, Appl
6	361	39.3	450	5	US-09-194-164-6 Sequence 6, Appl
7	359.4	39.2	450	5	US-09-194-164-4 Sequence 4, Appl
8	324.4	35.3	543	5	US-09-194-164-1 Sequence 1, Appl
9	324.4	35.3	543	5	US-09-194-164-3 Sequence 3, Appl
10	318.4	34.7	1680	1	PCT-US03-26232-15 Sequence 15, Appl
11	283.8	30.9	436	1	PCT-US03-26232-145 Sequence 45, Appl
12	282.8	30.8	324	1	PCT-US03-21304-42 Sequence 42, Appl
13	278.2	30.3	646	5	US-09-194-164-2 Sequence 2, Appl
14	276.2	30.1	351	1	PCT-US03-21304-4 Sequence 4, Appl
15	274.6	29.9	351	1	PCT-US03-21304-5 Sequence 5, Appl
16	274.6	29.9	351	1	PCT-US03-21304-6 Sequence 6, Appl
17	273.8	29.8	352	1	PCT-US03-25161-17 Sequence 17, Appl
18	273	29.7	351	1	PCT-US03-21304-7 Sequence 7, Appl
19	272.2	29.7	351	1	PCT-US03-21304-8 Sequence 8, Appl
20	271.6	29.6	324	1	PCT-US03-21304-43 Sequence 43, Appl
21	271.4	29.6	351	1	PCT-US03-21304-9 Sequence 9, Appl
22	270.4	29.5	351	1	PCT-US03-21304-10 Sequence 10, Appl
23	270.4	29.5	648	1	PCT-US03-10749A-47 Sequence 47, Appl
24	267.4	29.1	457	1	PCT-US03-26232-75 Sequence 75, Appl
25	267.4	29.1	648	1	PCT-US03-10749A-51 Sequence 51, Appl
26	267.4	29.1	747	1	PCT-US03-25457-65 Sequence 65, Appl

27	265.8	29.0	648	1	PCT-US03-10749A-31 Sequence 31, Appl
28	264.2	28.8	648	1	PCT-US03-10749A-39 Sequence 39, Appl
29	259.8	28.3	345	1	PCT-US03-21304-12 Sequence 12, Appl
30	258.2	28.1	345	1	PCT-US03-21304-15 Sequence 15, Appl
31	255	27.8	708	1	PCT-US02-26584-2 Sequence 2, Appl
32	253.4	27.6	345	1	PCT-US03-21304-13 Sequence 13, Appl
33	249.8	27.2	336	1	PCT-US03-21304-11 Sequence 11, Appl
34	249.2	27.1	327	1	PCT-US03-21304-44 Sequence 44, Appl
35	248.6	27.1	327	1	PCT-US03-10749A-23 Sequence 23, Appl
36	248.6	27.1	345	1	PCT-US03-21304-14 Sequence 14, Appl
37	248	27.0	318	1	PCT-US03-21304-46 Sequence 46, Appl
38	246.6	26.9	903	6	US-10-375-356A-12 Sequence 12, Appl
39	246.6	26.9	913	6	US-10-375-356A-10 Sequence 10, Appl
40	245.6	26.8	1430	1	PCT-US02-26584-1 Sequence 1, Appl
41	245.4	26.7	327	1	PCT-US03-10749A-27 Sequence 27, Appl
42	244.4	26.6	321	1	PCT-US03-21304-45 Sequence 45, Appl
43	244	26.6	324	1	PCT-US03-21304-48 Sequence 48, Appl
44	243.8	26.6	327	1	PCT-US03-10749A-7 Sequence 7, Appl
45	242.2	26.4	327	1	PCT-US03-10749A-15 Sequence 15, Appl

## ALIGNMENTS

RESULT 1  
US-09-194-164-13  
Sequence 13, Application US/09194164  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
Malti, Pradip K.  
Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT  
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/194,164  
FILING DATE: 09-Apr-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/657,449  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 918 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1..906, 913..918)  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:



```

OY 361 ACACCTCAGATCACTTTCGCGGAGGAGCAAGAGTGAGATCAAAACGAACTGGCTGCA 420
Db 558 ACACTCAGATCACTTTCGCGGAGGAGCAAGAGTGAGATCAAAACGAACTGGCTGCA 499
OY 421 CCATCTGCTCTCGCGGATGGCGGATTCGCGAGGTGGTGATCAAGTGGAGTGGCTCCAG 480
Db 498 CCATCTGCTCTCGCGGATGGCGGATTCGCGAGGTGGTGATCAAGTGGAGTGGCTCCAG 439
OY 481 GGGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCTGGGAGGTCCCTGAGACTCTCC 540
Db 438 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCTGGGAGGTCCCTGAGACTCTCC 379
OY 541 TGTGAGAGCTCTGGAATTCCTCTTCAGAACTCTTGCTATGCACTGGGTCCGCAAGCTCTA 600
Db 378 TGTGAGAGCTCTGGAATTCCTCTTCAGAACTCTTGCTATGCACTGGGTCCGCAAGCTCTA 319
OY 601 GGCAGAGGGGCTGAGTGGGTGGCAGTTATATATATATATGATGAGAGCACTAATACTACGCA 660
Db 318 GGCAGAGGGGCTGAGTGGGTGGCAGTTATATATATATATGATGAGAGCACTAATACTACGCA 259
OY 661 GACTCCGTGGAAGGGCCGATTCACCATCTCAGAGACACTTCCAAAGAACGGTGTATCTA 720
Db 258 GACTCCGTGGAAGGGCCGATTCACCATCTCAGAGACACTTCCAAAGAACGGTGTATCTA 199
OY 721 AAAATGAAACAGCCTGAGAACTGAGGACACGGCTGTATATCTGTCGAGAGATGACAGAC 780
Db 198 AAAATGAAACAGCCTGAGAACTGAGGACACGGCTGTATATCTGTCGAGAGATGACAGAC 139
OY 781 CTGTTGGGTGACTATGACCACTACTACCGGTTTGGACGTCTGGGGCAAAAGGACCAAGCTC 840
Db 138 CTGTTGGGTGACTATGACCACTACTACCGGTTTGGACGTCTGGGGCAAAAGGACCAAGCTC 79
OY 841 ACCGTCTCTCAGAGATCCGAAACAAACCTGATCAGGAAAGATCTGAACCATCAACCT 900
Db 78 ACCGTCTCTCAGAGATCCGAAACAAACCTGATCAGGAAAGATCTGAACCATCAACCT 19
OY 901 CACCATTAAGTGAAGCTT 918
Db 18 CACCATTAAGTGAAGCTT 1

RESULT 3
US-09-194-164-16
: Sequence 16, Application US/09194164
: GENERAL INFORMATION:
: APPLICANT: Dan, Michael D.
: Mailli, Pradi K.
: Kaplan, Howard A.
: TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT
: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
: DETECTION OF CANCERS
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Morrison & Foerster
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/194,164
: FILING DATE: 09-Apr-1999
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/657,449
: FILING DATE: <Unknown>

```

[illegible]

Db 670 AAATGAACAGCCTGAGAACTGAGACACGCGTGTCTATTACTGTCTCGAGAGATCAGAAC 729

Qy 781 CTGTGGGTGACATATGACCACTACTACGTTTGGAGCTGGGGCAAGGACACAGCTC 840

Db 730 CTGTGGGTGACATATGACCACTACTACGTTTGGAGCTGGGGCAAGGACACAGCTC 789

Qy 841 ACCGTCCTCAGAGATCCGAAACAAATCTGATCAGGAGAGATCTGAACATCAACAT 900

Db 790 ACCGTCCTCAGAGATCCGAAACAAATCTGATCAGGAGAGATCTGAACATCAACAT 849

Qy 901 CACCATTAAGTGAAGCTT 918

Db 850 CACCATTAAGTGAAGCTT 867

RESULT 4

US-09-194-164-18/c

Sequence 18, Application US/09194164

GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

Maifi, Pradip K.

Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/194,164

FILING DATE: 09-Apr-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/657,449

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 867 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-194-164-18

Query Match 86.9%; Score 798; DB 5; Length 867;

Best Local Similarity 93.9%; Pred. No. 5,4e-223;

Matches 862; Conservative 0; Mismatches 5; Indels 51; Gaps 1;

Qy 1 GAATTATGAAAAAACCCTATTCGGATCGGAGTGGACCTGGCTTCCCTACCGT 60

Db 867 GAATTCATATAAAAAACCGCTATCGGATCGGAGTGGACCTGGCTTCCCTACCGT 808

Qy 61 GCGCAGGCGCATTTGTGTGACGAGTCTCCAGGACCCCTGTTTGTCTCCAGGGGAA 120

Db 807 GCGCAGGCGCATTTGTGTGACGAGTCTCCAGGACCCCTGTTTGTCTCCAGGGGAA 748

Qy 121 AGAGCACCCTCTCTCGAGGGCCAGATCAGATGTATGATGACCTACTTAAAGCTGTAC 180

Db 747 AGAGCACCCTCTCTCGAGGGCCAGATCAGATGTATGATGACCTACTTAAAGCTGTAC 688

Qy 181 CAGCAAAACCTGGCAGAGCTCCAGAGCTCTCATATATGATGATCCACAGGGGCACT 240

Db 687 CAGCAAAACCTGGCAGAGCTCCAGAGCTCTCATATATGATGATCCACAGGGGCACT 628

Qy 241 GGCATGCCAGACAGGTTGATGAGAGTGGTCCGGGACAGACTTCACTTCACTCACTAGT 300

Db 627 GGCATGCCAGACAGGTTGATGAGAGTGGTCCGGGACAGACTTCACTTCACTCACTAGT 568

Qy 301 AGACTGAGCTGAAAGATTTTGCAGTGTATTAATCTGACAGATGATGATGATGATGAT 360

Db 567 AGACTGAGCTGAAAGATTTTGCAGTGTATTAATCTGACAGATGATGATGATGATGAT 508

Qy 361 ACACCTCAGATCACTTTCGCGGAGGACCAAGTGAGATCAAAAGAACTGTGGCTGCA 420

Db 507 ACACCTCAGATCACTTTCGCGGAGGACCAAGTGAGATCAAAAGAACTGTGGCTGCA 448

Qy 421 CCATCTGTCTTGGCGGTGGCGGTTCCGAGGTGTGATCAGTGGAGTGGCTCCAG 480

Db 447 TC-----CGACAG 439

Qy 481 GTGCAGCTGTGATGATCTGGGGGAGCGTGTCCAGCTGGAGGCTCCCTGAGACTCC 540

Db 438 GTGCAGCTGTGATGATCTGGGGGAGCGTGTGTGATGATGATGATGATGATGATGATG 379

Qy 541 TGTGACGCTGTGATGATCTGCTTCAAGACTTGTGATGATGATGATGATGATGATGATG 600

Db 378 TGTGACGCTGTGATGATCTGCTTCAAGACTTGTGATGATGATGATGATGATGATGATG 319

Qy 601 GGCAGGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660

Db 318 GGCAGGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 259

Qy 661 GATCGGTGAAAGGCGGATTCACATCTCCAGAGACCTTCCAGAAACAGGTTATCTTA 720

Db 258 GATCGGTGAAAGGCGGATTCACATCTCCAGAGACCTTCCAGAAACAGGTTATCTTA 199

Qy 721 AAATGAACAGCCTGAGAACTGAGACACGCGTGTCTATTACTGTGCGAGATCAGAAC 780

Db 198 AAATGAACAGCCTGAGAACTGAGACACGCGTGTCTATTACTGTGCGAGATCAGAAC 139

Qy 781 CTGTGGGTGACATATGACCACTACTACGTTTGGAGCTGGGGCAAGGACACAGCTC 840

Db 138 CTGTGGGTGACATATGACCACTACTACGTTTGGAGCTGGGGCAAGGACACAGCTC 79

Qy 841 ACCGTCCTCAGAGATCCGAAACAAATCTGATCAGGAGAGATCTGAACATCAACAT 900

Db 78 ACCGTCCTCAGAGATCCGAAACAAATCTGATCAGGAGAGATCTGAACATCAACAT 19

Qy 901 CACCATTAAGTGAAGCTT 918

Db 18 CACCATTAAGTGAAGCTT 1

RESULT 5

PCT-US03-14964-4

Sequence 4, Application PC/TUS0314964

GENERAL INFORMATION:

APPLICANT: Rother, Russell P

Geis, David R

TITLE OF INVENTION: T7 Bacteriophage Display of Fabs

FILE REFERENCE: 1087-24 PCT

CURRENT APPLICATION NUMBER: PCT/US03/14964

CURRENT FILING DATE: 2003-07-17

PRIOR APPLICATION NUMBER: US 60/380,318

PRIOR FILING DATE: 2002-05-14

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 4  
 LENGTH: 1103  
 TYPE: DNA  
 ORGANISM: human  
 PCT-US03-14964-4

Query Match 49.8%; Score 457; DB 1; Length 1103;  
 Best Local Similarity 74.3%; Pred. No. 2.1e-123;  
 Matches 628; Conservative 0; Mismatches 190; Indels 27; Gaps 3;

```

QY 7 ATGAAAAAACCGCTATTCGGATCGCATGTCCTGGCTGGTTCCCTACCGTGGCCAG 66
DB 210 ATGAAAAAACAGCTATCCGATGAGGCACTGGCTGGTTCCCTACCGTGGCCAG 269
QY 67 GCGCATATGTTGTCAGGAGTCTCCAGGCACTCTGTTGTCCTCAGGGGAAAGAGCC 126
DB 270 GCGG---CCGAGCTACGAGTCTCCAGGCACTCTGTTGTCCTCAGGGGAAAGAGCC 326
QY 127 ACCCTCTCTGCAAGGCGCAGTCAGAGTGTAGAGAGCTTACCTGTACAGCAG 186
DB 327 ACCCTCTCTGCAAGGCGCAGTCAGAGTGTAGAGAGCTTACCTGTACAGCAG 386
QY 187 AAACCTGGCGAGGCTCCGAGGCTCTCATCTATGTCATCCAGGGCCACTGGCAGT 246
DB 387 AAACCTGGCGAGGCTCCGAGGCTCTCATCTATGTCATCCAGGGCCACTGGCAGT 446
QY 247 CCAGACAGGTTGAGTGGCAGTGGGTCGGGACAGCTTCACTCTCAGTCAGTAGAGT 306
DB 447 CCAGACAGGTTGAGTGGCAGTGGGTCGGGACAGCTTCACTCTCAGTCAGTAGAGT 506
QY 307 GAGCCTGAAGATTTGTCAGTGTATTACTGTACAGCAGTATGAGTCACTCAGACAG 366
DB 507 GAGCCTGAAGATTTGTCAGTGTATTACTGTACAGCAGTATGAGTCACTCAGAGT 560
QY 367 CAGATCACTTTGGCGGAGGAGCAGAGTGTAGATCAAGAGCTGTGGCTGCACATCT 426
DB 561 -----TTGCGCCAGAGGAGCAGAGTGTAGATCAAGAGCTGTGGCTGCACATCT 611
QY 427 GTCTGTGGGCGGTGGCGGTTCCGAGGTTGAGTCAAGTGGTGGCTCCAGAGTGCAG 486
DB 612 GCGTGGGCGGT-----GGTGGGCGGTGGCTCTTGAATCTTCCAGAGTGCAGTGC 662
QY 487 CTGTGTGAGTCTGGGAGGAGCGGTGTCAAGCCTGGAGAGTCCCTGAGACTTCTGTGCA 546
DB 663 CTGTGTGAGTCTGGGAGGAGCGGTGTCAAGCCTGGAGAGTCCCTGAGACTTCTGTGCA 722
QY 547 GCGTGTGAGTCCCTTCAAGAACTTGTGTATGCACTGGGTCGCGAGGCTTGAAGCAAG 606
DB 723 GCGTGTGAGGAGCACTTCAAAATATGTCATGCACTGGGTCGAGAGGCGCCCTGAGCAA 782
QY 607 GGGCTGAGTGGGTGGCAGTATATCATATGATGAGAGCACTAAATCAACGAGACTCC 666
DB 783 GGGCTGAGTGGGTGGCAGTATATCATATGATGAGAGCACTAAATCAACGAGACTCC 842
QY 667 GTGAAGGCGCGATTCAACATCTCCAGAGACACTTCCAGAGACGCGTGTATCTAAATG 726
DB 843 TTCCAGGGGAGAGTCAACATTCGCGGAGAGATCCACGGGCAACGCTCAATGAGCTG 902
QY 727 AACAGCTGAGAACTGAGAGCAACGCGTGTCTATTACTGTGCGAGAGATCAAGGCTGTTG 786
DB 903 AACAGCTGAGAACTGAGAGCAACGCGTGTCTATTACTGTGCGAGAGATCAAGGCTGTTG 962
QY 787 GGTGATATGACACACTACGTTTGGAGCTGTGGGCGAAAGGAGCAACGCTCAACCGTC 846
DB 963 GGTGATATGACACACTACGTTTGGAGCTGTGGGCGAAAGGAGCAACGCTCAACCGTC 1022
QY 847 TCCTC 851
DB 1023 TCAC 1027

```

RESULT 6

US-09-194-164-6/c  
 Sequence 6, Application US/09194164  
 GENERAL INFORMATION:  
 APPLICANT: Dan, Michael D.  
 Maitl, Pradip K.  
 Kaplan, Howard A.  
 TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Morrison & Foerster  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304-1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/194,164  
 FILING DATE: 09-Apr-1999  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/657,449  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Leinhardt, Susan K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 31608-20001.00  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 450 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 US-09-194-164-6

Query Match 39.3%; Score 361; DB 5; Length 450;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-95;  
 Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 70 GATATGTGTGACGACAGTCTCCAGGACCCCTGTTGTCTCCAGGGGAAAGAGCCAGC 129
DB 378 GATATGTGTGACGACAGTCTCCAGGACCCCTGTTGTCTCCAGGGGAAAGAGCCAGC 319
QY 130 CTCTCTGAGGCGCAGTCAAGAGTGTAGTACAGTACTTACCTGTGATCCAGAGAA 189
DB 318 CTCTCTGAGGCGCAGTCAAGAGTGTAGTACAGTACTTACCTGTGATCCAGAGAA 259
QY 190 CTTGCGCAGGCTCCAGAGCTCTCATCTATGAGTGCATCCAGGAGCCACTGGCATGCCA 249
DB 258 CTTGCGCAGGCTCCAGAGCTCTCATCTATGAGTGCATCCAGGAGCCACTGGCATGCCA 199
QY 250 GACAGGTTCAAGTGGAGTGGTCCGGGACAGACTTCACTCTCAACATAGTAGACTGGAG 309
DB 198 GACAGGTTCAAGTGGAGTGGTCCGGGACAGACTTCACTCTCAACATAGTAGACTGGAG 139
QY 310 CCTGAAGATTTGCAAGTGTATGTCAGCAGTATGAGTGTGAGTGTGAGTGTGAGTGTGAG 369
DB 138 CCTGAAGATTTGCAAGTGTATGTCAGCAGTATGAGTGTGAGTGTGAGTGTGAGTGTGAG 79
QY 370 ATCACTTTGCGGAGGAGCAAGGTGAGATCAAGAGCTGTGGCTGACCATCTGTCTC 429

```

Db 78 ATCACTTTCGGCGAGGACCAAGGTGAGATCAAGCACTGTGGCTGCACCATCTGTC 19  
QY 430 T 430  
Db 18 T 18

RESULT 7  
US-09-194-164-4

Sequence 4, Application US/09194164

GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

Maiti, Pradip K.

Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT

SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE

FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND

DETECTION OF CANCERS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/194.164

FILING DATE: 09-Apr-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/657.449

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 450 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 1..450

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-194-164-4

Query Match 39.2%; Score 359.4; DB 5; Length 450;

Best Local Similarity 99.7%; Pred. No. 4.7e-95;

Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 70 GATATTGTGTGAGCGAGTCTCCAGGACCCCTGCTTGTCTCCAGGGGAAAGGCCACC 129

Db 73 GATTTGTGTGAGCGAGTCTCCAGGACCCCTGCTTGTCTCCAGGGGAAAGGCCACC 132

QY 130 CTCTCTGCAAGGCGCACTGAGGTGTTAGTACGCTACTTACCTGTTACGAGGAAA 189

Db 133 CTCTCTGCAAGGCGCACTGAGGTGTTAGTACGCTACTTACCTGTTACGAGGAAA 192

QY 190 CCGGCGAGGCTCCCGAGGCTCTCATATGATGTCATCCACGAGGCGCATCTGGATGCCA 249

Db 193 CCGGCGAGGCTCCCGAGGCTCTCATATGATGTCATCCACGAGGCGCATCTGGATGCCA 252

QY 250 GACAGGTTGATGCGCAGTGGGTCGCGACAGACTTCACTCTCAACATCACTAGACCTGGAG 309  
Db 253 GACAGGTCACAGTGGGTCGCGACAGACTTCACTCTCAACATCACTAGACCTGGAG 312  
QY 310 CCGAAGATTTCAGATGATTAATCTGACAGCACTATGTTAGTACCTGACCTGACACCTCAG 369  
Db 313 CCGAAGATTTCAGATGATTAATCTGACAGCACTATGTTAGTACCTGACCTGACACCTCAG 372  
QY 370 ATCACTTCGCGAGGAGCAAGGTGAGATCAAGCACTGCTGCTGACCATCTGTC 429  
Db 373 ATCACTTCGCGAGGAGCAAGGTGAGATCAAGCACTGCTGCTGACCATCTGTC 432  
QY 430 T 430  
Db 433 T 433

RESULT 8

US-09-194-164-1

Sequence 1, Application US/09194164

GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

Maiti, Pradip K.

Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT

SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE

FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND

DETECTION OF CANCERS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/194.164

FILING DATE: 09-Apr-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/657.449

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 543 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 1..543

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-194-164-1

Query Match

Best Local Similarity

Matches 349; Conservative

35.3%; Score 324.4; DB 5; Length 543;

89.3%; Pred. No. 8.4e-85;

0; Mismatches 42; Indels 0; Gaps 0;

QY 440 GCGGTTCCGAGAGTGTGATCAGGTGAGGTGGCTCCAGGTCAGCTGTGTGAGTCTG 499  
 Db 152 GGGTTTCTCTGCTTCTTTTAAGAGTATCCAGGTGAGGTGAGCTGTGTGAGTCTG 211  
 QY 500 GGGGAGGCGGTGTGTCAGGCTGGAGAGTCCCTGAGATCTCCGTGTGAGCTGTGATTC 559  
 Db 212 GGGGAGGCGGTGTGTCAGGCTGGAGAGTCCCTGAGATCTCCGTGTGAGCTGTGATTC 271  
 QY 560 CCTTGAAGACTTTGTATGCACTGGGTCGCGCAGGCTTGAAGCAAGGGCTGAGTGG 619  
 Db 272 CTTGAGAGCTTTGTATGCACTGGGTCGCGCAGGCTTGAAGCAAGGGCTGAGTGG 331  
 QY 620 TGGCAGTTATCATATGATGAGACATAAATACTAGCACTCCGTGAAGGCCGAT 679  
 Db 332 TGGCAGTTATCATATGATGAGACATAAATACTAGCACTCCGTGAAGGCCGAT 391  
 QY 680 TCACCATCTCCAGAGACCTTCCAGAGACGGTGTATTAATAAATGAACAGCTGAGAA 739  
 Db 392 TCACCATCTCCAGAGACCTTCCAGAGACGGTGTATTAATAAATGAACAGCTGAGAA 451  
 QY 740 CTGAGAGACGGCTGTCTATCTGTGCGAGAGATCAGAGCTGTGGTGAATATGACC 799  
 Db 452 CTGAGAGACGGCTGTCTATCTGTGCGAGAGATCAGAGCTGTGGTGAATATGACC 511  
 QY 800 ACTACTACGGTTTGAAGCTGTGGGCAAGG 830  
 Db 512 ACTACTACGGTTTGAAGCTGTGGGCAAGG 542

## RESULT 9

US-09-194-164-3/c  
 ; Sequence 3, Application US/09194164  
 ; GENERAL INFORMATION:

APPLICANT: Dan, Michael D.  
 ;

Malet, Pradip K.  
 ;

Kaplan, Howard A.  
 ;

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT  
 SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
 FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
 DETECTION OF CANCERS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:  
 ;

ADDRESSEE: Morrison & Foerster  
 ;

STREET: 755 Page Mill Road  
 ;

CITY: Palo Alto  
 ;

STATE: CA  
 ;

COUNTRY: USA  
 ;

ZIP: 94304-1018  
 ;

COMPUTER READABLE FORM:  
 ;

MEDIUM TYPE: Floppy disk  
 ;

COMPUTER: IBM PC compatible  
 ;

OPERATING SYSTEM: PC-DOS/MS-DOS  
 ;

SOFTWARE: Patentin Release #1.0, Version #1.30  
 ;

CURRENT APPLICATION DATA:  
 ;

APPLICATION NUMBER: US/09/194,164  
 ;

FILING DATE: 09-Apr-1999  
 ;

CLASSIFICATION: <Unknown>  
 ;

PRIOR APPLICATION DATA:  
 ;

APPLICATION NUMBER: US/08/657,449  
 ;

FILING DATE: <Unknown>  
 ;

ATTORNEY/AGENT INFORMATION:  
 ;

NAME: Lehnhardt, Susan K.  
 ;

REGISTRATION NUMBER: 33,943  
 ;

REFERENCE/DOCKET NUMBER: 31608-20001.00  
 ;

TELECOMMUNICATION INFORMATION:  
 ;

TELEPHONE: (415) 813-5600  
 ;

TELEFAX: (415) 494-0792  
 ;

TELEX: 706141  
 ;

INFORMATION FOR SEQ ID NO: 3:  
 ;

SEQUENCE CHARACTERISTICS:  
 ;

LENGTH: 543 base pairs  
 ;

TYPE: nucleic acid  
 ;

STRANDEDNESS: double  
 ;

TOPOLOGY: linear  
 ;  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 ; US-09-194-164-3

Query Match 35.3%; Score 324.4; DB 5; Length 543;  
 Best Local Similarity 89.3%; Pred. No. 8,4e-85;  
 Matches 349; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 440 GCGGTTCCGAGAGTGTGATCAGGTGAGGTGGCTCCAGGTCAGCTGTGTGAGTCTG 499  
 Db 392 GGGTTTCTCTGCTTCTTTTAAGAGTATCCAGGTGAGGTGAGCTGTGTGAGTCTG 333  
 QY 500 GGGGAGGCGGTGTGTCAGGCTGGAGAGTCCCTGAGATCTCCGTGTGAGCTGTGATTC 559  
 Db 332 GGGGAGGCGGTGTGTCAGGCTGGAGAGTCCCTGAGATCTCCGTGTGAGCTGTGATTC 273  
 QY 560 CCTTGAAGACTTTGTATGCACTGGGTCGCGCAGGCTTGAAGCAAGGGCTGAGTGG 619  
 Db 272 CTTGAGAGCTTTGTATGCACTGGGTCGCGCAGGCTTGAAGCAAGGGCTGAGTGG 213  
 QY 620 TGGCAGTTATCATATGATGAGACATAAATACTAGCACTCCGTGAAGGCCGAT 679  
 Db 212 TGGCAGTTATCATATGATGAGACATAAATACTAGCACTCCGTGAAGGCCGAT 153  
 QY 680 TCACCATCTCCAGAGACCTTCCAGAGACGGTGTATTAATAAATGAACAGCTGAGAA 739  
 Db 152 TCACCATCTCCAGAGACCTTCCAGAGACGGTGTATTAATAAATGAACAGCTGAGAA 93  
 QY 740 CTGAGAGACGGCTGTCTATCTGTGCGAGAGATCAGAGCTGTGGTGAATATGACC 799  
 Db 92 CTGAGAGACGGCTGTCTATCTGTGCGAGAGATCAGAGCTGTGGTGAATATGACC 33  
 QY 800 ACTACTACGGTTTGAAGCTGTGGGCAAGG 830  
 Db 32 ACTACTACGGTTTGAAGCTGTGGGCAAGG 2

## RESULT 10

PCT-US03-14964-1  
 ; Sequence 1, Application PC/TUS0314964

GENERAL INFORMATION:  
 ;

APPLICANT: Rother, Russell P  
 ;

APPLICANT: Geis, David R  
 ;

TITLE OF INVENTION: T7 Bacteriophage Display of Fabs  
 ;

FILE REFERENCE: 1087-24 PCT  
 ;

CURRENT APPLICATION NUMBER: PCT/US03/14964  
 ;

CURRENT FILING DATE: 2003-07-17  
 ;

PRIOR APPLICATION NUMBER: US 60/380,318  
 ;

PRIOR FILING DATE: 2002-05-14  
 ;

NUMBER OF SEQ ID NOS: 16  
 ;

SOFTWARE: Patentin version 3.2  
 ;

SEQ ID NO 1  
 ;

LENGTH: 1680  
 ;

TYPE: DNA  
 ;

ORGANISM: human  
 ;

PCT-US03-14964-1  
 ;

Query Match 34.7%; Score 318.4; DB 1; Length 1680;  
 Best Local Similarity 88.4%; Pred. No. 7,2e-83;  
 Matches 375; Conservative 0; Mismatches 31; Indels 18; Gaps 2;

QY 7 ATGAAAAAACCGCATCGCATCGCATGTCGCTGTTGCGTACCGTGGCGAG 66  
 Db 7 ATGAAAAAACCGCATCGCATCGCATGTCGCTGTTGCGTACCGTGGCGAG 66  
 QY 67 GCGAATTTGTGTGATGCGAGTCTCCAGGACCTGTCTTTGTCTTCAGGGAAAGAGCC 126  
 Db 67 GCGG---CCGAGCTCAGCGAGTCTCCAGGACCTGTCTTTGTCTTCAGGGAAAGAGCC 123  
 QY 127 ACCCTCTCTGAGGGCAGTCAAGTGTAGAGTGTAGAGTCTTGGTCCGTGACCGAG 186  
 Db 124 ACCCTCTCTGAGGGCAGTCAAGTGTAGAGTGTAGAGTCTTGGTCCGTGACCGAG 183

QY 187 AAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGATCATCCAGGCGCACTGGAGT 246  
| | | | |  
DB 184 AAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGATCATCCAGGCGCACTGGAGT 243  
| | | | |  
QY 247 CCAGACAGGTTCACTGAGTGGAGTGGGTCGGGACAGACTTCACTCTACCATCTAGTAGT 306  
| | | | |  
DB 244 CCAGACAGGTTCACTGAGTGGAGTGGGTCGGGACAGACTTCACTCTACCATCTAGTAGT 303  
| | | | |  
QY 307 GAGCCTGAAGATTTTGAAGTATATCTATGTCAGAGATGAGTGTAGTCACTGACACACT 366  
| | | | |  
DB 304 GAGCCTGAAGATTTTGAAGTATATCTATGTCAGAGATGAGTGTAGTCACTGACACACT 357  
| | | | |  
QY 367 CAGATCACTTTCGGCGGAGGACCAAGGTGAGATCAACGACTGTGCTGACCATCT 426  
| | | | |  
DB 358 -----TTCCGCCAAGGACCAAGGTGAGATCAACGACTGTGCTGACCATCT 408  
| | | | |  
QY 427 GTCT 430  
| | | | |  
DB 409 GTCT 412

## RESULT 11

PCT-US03-26232-145  
; Sequence 145, Application PC/TUS0326232  
; GENERAL INFORMATION:  
; APPLICANT: ABGENIX, INC.  
; APPLICANT: GUIDAS, Jean M.  
; APPLICANT: HAAR-FRENDSCHO, Mary  
; APPLICANT: FOORD, Orlie  
; APPLICANT: LIANG, Meina L.  
; APPLICANT: AHUMVALLIA, Kiran  
; APPLICANT: BHAKTA, Sunil  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE  
; FILE REFERENCE: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF  
; CURRENT APPLICATION NUMBER: PCT/US03/26232  
; PRIOR FILING DATE: 2003-08-19  
; PRIOR APPLICATION NUMBER: US 60/404,802  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 145  
; LENGTH: 436  
; TYPE: DNA  
; ORGANISM: Homosapien  
PCT-US03-26232-145

## Query Match

Best Local Similarity 30.9%; Score 283.8; DB 1; Length 436;  
Matches 325; Conservative 0; Mismatches 32; Indels 12; Gaps 1;

QY 490 GTGAGTCTGGGGGAGGCGTGTCTCAGCTGGAGGTCCTCTGAGACTCTCTCTGTGCGGCC 549  
| | | | |  
DB 1 GACACAGTCGGGGGAGGCGTGTCTCAGCTGGAGGTCCTCTGAGACTCTCTCTGTGCGGCC 60  
| | | | |  
QY 550 TCTGATTTCCCTCAGAACTTTGCTATGCACTGGGTCGGCCAGGCTTACGCAAGGAG 609  
| | | | |  
DB 61 TCTGATTTCCCTCAGAACTTTGCTATGCACTGGGTCGGCCAGGCTTACGCAAGGAG 120  
| | | | |  
QY 610 CTGAGTGGTGGGAGTATATCATATGATGAGACCTAAATCTACGACACTCCGTG 669  
| | | | |  
DB 121 CTGAGTGGTGGGAGTATATGATGATGAGAAATATAAATCTATGAGACTCCGTG 180  
| | | | |  
QY 670 AAGGCGGATTCACCATCTCCAGAGACACTTCCAGAAACGCGTGTCTTAAATGAAC 729  
| | | | |  
DB 181 AAGGCGGATTCACCATCTCCAGAGACACTTCCAGAAACGCGTGTCTTAAATGAAC 240  
| | | | |  
QY 730 AGCTGAGACTGAGACAGGCGTGTCTATCTATGTCGAGAGATCAGAGCTGTGGGT 789  
| | | | |  
DB 241 AGCTGAGACTGAGACAGGCGTGTCTATCTGTGAGAGATCAGAGCTGTGGGT 295  
| | | | |  
QY 790 GACTATGACCACTACTAGCTGTGGAGCTGTGGGCAAGGAGCAAGCTCACCGTCTCC 849  
| | | | |

DB 296 -----ACTACTACTAGGATGAGCTGTGGGCGCAAGGAGCAAGGTCACTGCTCC 348  
| | | | |  
QY 850 TCAGATCC 858  
| | | | |  
DB 349 TCAGCTCC 357  
| | | | |

## RESULT 12

PCT-US03-21304-42  
; Sequence 42, Application PC/TUS0321304  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET  
; FILE REFERENCE: 053893-5050MO  
; CURRENT APPLICATION NUMBER: PCT/US03/21304  
; CURRENT FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,356  
; PRIOR FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/411,694  
; PRIOR FILING DATE: 2003-09-18  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 42  
; LENGTH: 324  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US03-21304-42

## Query Match

Best Local Similarity 30.8%; Score 282.8; DB 1; Length 324;  
Matches 312; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

QY 70 GATATTGTGTGACGAGTCTCCAGGACCCCTGTTGTCTCTCCAGGGAAGAGCCACC 129  
| | | | |  
DB 1 GAATATTGTGTGACAGTCTCCAGGACCCCTGTTGTCTCTCCAGGGAAGAGCCACC 60  
| | | | |  
QY 130 CTCTCCGAGGCGGCGAGTCAAGATGTTAGAGGAGTCTAGCTGTGTCAGAGAA 189  
| | | | |  
DB 61 CTCTCCGAGGCGGCGAGTCAAGATGTTAGAGGAGTCTAGCTGTGTCAGAGAA 120  
| | | | |  
QY 190 CTTGGCAGGCTCCAGGCTCTCATCTATGTCATCCAGAGGCGCACTGGCATGCCA 249  
| | | | |  
DB 121 CTTGGCAGGCTCCAGGCTCTCATCTATGTCATCCAGAGGCGCACTGGCATGCCA 180  
| | | | |  
QY 250 GACAGGTCAGTGGGTCGGGTCGGGACAGACTTCACTCACTAGTATAGTGAAG 309  
| | | | |  
DB 181 GACAGGTCAGTGGGTCGGGTCGGGACAGACTTCACTCACTAGTATAGTGAAG 240  
| | | | |  
QY 310 CTTGAAGATTTTCACTGATCTATCTGTCAGCAGTATGTCACCTCAGACACTCAG 369  
| | | | |  
DB 241 CTTGAAGATTTTCACTGATCTATCTGTCAGCAGTATGTCACCTCAGACACTCAG 289  
| | | | |  
QY 370 ATCACTTTCGGCGAGGAGCAAGGTGAGATCAAA 405  
| | | | |  
DB 290 -TCACCTTTCGGCGAGGAGCAAGGTGAGATCAAA 324  
| | | | |

## RESULT 13

US-09-610-551B-2  
; Sequence 2, Application US/09610551B  
; GENERAL INFORMATION:  
; APPLICANT: Barbas, Carlos F. III  
; APPLICANT: Burton, Dennis R.  
; APPLICANT: Lerner, Richard A.  
; TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES  
; USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS  
; NUMBER OF SEQUENCES: 70  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute  
; STREET: 10666 North Torrey Pines Road, TPC8  
; CITY: La Jolla  
; STATE: CA



```

; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,551B
; FILING DATE: 05-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/826,623
; FILING DATE: 27-JAN-1992
; APPLICATION NUMBER: US 08/174,674
; FILING DATE: 28-DEC-1993
; APPLICATION NUMBER: US 08/300,386
; FILING DATE: 02-SEP-1994
; APPLICATION NUMBER: US 08/931,645
; FILING DATE: 16-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 409.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-554-2937
; TELEFAX: 858-554-6312
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 646 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-610-551B-2

Query Match      30.3%; Score 278.2; DB 5; Length 646;
Best Local Similarity 89.3%; Pred. No. 2,7e-71;
Matches 317; Conservative 0; Mismatches 23; Indels 15; Gaps 1;

QY 76 GTGTGACGACGCTTCACGACACCCGTGTTGTCTCCAGGGGAAAGACCCCTCTCC 135
DB 1 GAGCTCAGCAGCTTCACGACACCCGTGTTGTCTCCAGGGGAAAGACCCCTCTCC 60
QY 136 TCCAGGGCCAGTCAAGTGTGTAGTACAGCTACTTACCTGGTGAACAGAAAGCTGGC 195
DB 61 TCCAGGGCCAGTCAAGTGTGTAGTACAGGGGCTTACTTACCTGGTGAACAGAAAGCTGGC 120
QY 196 CAGGCTCCAGGCTCCTCATCTATGTGTGATCCACAGGGGCACTGGCAGTGCAGAG 255
DB 121 CAGGCTCCAGGCTCCTCATCTATGTGTGATCCACAGGGGCACTGGCAGTGCAGAG 180
QY 256 TTCAAGTGCAGTGTGTCCGGAAGAGCTTCACTCTCCAGCATGAGTGAAGCTGGA 315
DB 181 TCCAGTGCAGTGTGTGTGGGACAGACTTCACTCTCAACATCAGCAGATGGAAGCTGGA 240
QY 316 GATTTTGCAGTGTATTAATCTGTCAAGCAGTATGTAGTCACTCACTCAGACACCTCAATCACT 375
DB 241 GATTTTGCAGTGTATTAATCTGTCAAGCAGTATGTAGTCACTCACTCAGACACCTCAATCACT 285
QY 376 TTCCGCGGAGGAGCCAAAGGTGAGATCAAGAAAGTGGGCTGACCATCTGTCT 430
DB 286 TTCCGCGGAGGAGCCAAAGGTGAGATCAAGAAAGTGGGCTGACCATCTGTCT 340

RESULT 14
PCT-US03-21304-4
; Sequence 4, Application PC/TUS0321304
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
```

```

; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; FILE REFERENCE: 053893-5050MO
; CURRENT APPLICATION NUMBER: PCT/US03/21304
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,356
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2003-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 4
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-21304-4

Query Match      30.1%; Score 276.2; DB 1; Length 351;
Best Local Similarity 95.6%; Pred. No. 8.4e-71;
Matches 284; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 478 CAGGTGACGCTGTGAGTCTGGGGAGGCGGTGTCAGGCTGGAGAGTCCCGAGACTC 537
DB 1 CAGGTGACGCTGTGAGTCTGGGGAGGCGGTGTCAGGCTGGAGAGTCCCGAGACTC 60
QY 538 TCCGTGACGCTCTGGAATTCCTCTTCAAGACCTTGTCTATGACACTGGGTCCGAGGCT 597
DB 61 TCCGTGACGCTCTGGAATTCCTCTTCAAGACCTTGTCTATGACACTGGGTCCGAGGCT 120
QY 598 CTAGGCAAGGGGCTGTGAGTGGGTGGCAGTTATATCATATGANGAAGCACTAATATCTAC 657
DB 121 CCAGGCAAGGGGCTGTGAGTGGGTGGCAGTTATATCATATGANGAAGCACTAATATCTAC 180
QY 658 GCAGACTCCGTGAAGGCGGATTCACATCTCCAGAGACCTCCAGAAACAGGGGTAT 717
DB 181 GCAGACTCCGTGAAGGCGGATTCACATCTCCAGAGACCTCCAGAAACAGGGGTAT 240
QY 718 CTAAATGAACAGGCTGAGAACTGAGGACAGGCTGTCTATTACTGTGCGAGAGAT 774
DB 241 CTGCAATGAACAGGCTGAGAACTGAGGACAGGCTGTCTATTACTGTGCGAGAGAT 297

RESULT 15
PCT-US03-21304-5
; Sequence 5, Application PC/TUS0321304
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; FILE REFERENCE: 053893-5050MO
; CURRENT APPLICATION NUMBER: PCT/US03/21304
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,356
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2003-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 5
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-21304-5

Query Match      29.9%; Score 274.6; DB 1; Length 351;
Best Local Similarity 95.3%; Pred. No. 2.5e-70;
Matches 283; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 478 CAGGTGACGCTGTGAGTCTGGGGAGGCGGTGTCAGGCTGGAGAGTCCCGAGACTC 537
DB 1 CAGGTGACGCTGTGAGTCTGGGGAGGCGGTGTCAGGCTGGAGAGTCCCGAGACTC 60
QY 538 TCCGTGACGCTCTGGAATTCCTCTTCAAGACCTTGTCTATGACACTGGGTCCGAGGCT 597
```

